

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 01:57:11 ; Search time 5413.87 Seconds  
(without alignments)  
9562.892 Million cell updates/sec

Title: US-09-763-957-3  
Perfect score: 2474  
Sequence: 1 ttacagatacacagaatcag.....taacacatacacacatatgg 2474

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*  
29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htgo.inv.\*

C	1	147.4	5.0	86827	3	PFMAL3P5	AL034556 Plasmodiu
C	2	144.4	5.8	67970	3	PFMALIP3	AL031746 Plasmodiu
C	3	144.4	5.8	172816	3	AC093899	AC093899 Homo sapi
C	4	143.6	5.8	4601	3	DMU11584	U11584 Drosophila
C	5	143.6	5.8	19517	3	DMU37541	U37541 Drosophila
C	6	142.6	5.8	159618	9	AC096750	AC096750 Homo sapi
C	7	141.4	5.7	172724	2	AC098590	AC098590 Homo sapi
C	8	140.8	5.7	159618	9	AC096750	AC096750 Homo sapi
C	9	138.2	5.6	67970	3	PFMALIP3	AL031746 Plasmodiu
C	10	137.8	5.6	168698	9	AC068138	AC068138 Homo sapi
C	11	136.8	5.5	349980	6	AX344555	AX344555 Sequence
C	12	136.6	5.5	14867	3	AE001398	AE001398 Plasmodiu
C	13	136.6	5.5	104992	2	AC005504	AC005504 Plasmodiu
C	14	136.6	5.5	169546	2	AC004157	AC004157 Plasmodiu
C	15	136.4	5.5	104992	2	AC005504	AC005504 Plasmodiu
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C	18	136.2	5.5	326924	2	AC093082	AC093082 Homo sapi
C	19	135	5.5	181792	2	AC098822	AC098822 Homo sapi
C	20	134.2	5.4	205130	2	AC105425	AC105425 Homo sapi
C	21	133.6	5.4	155106	2	AC104069	AC104069 Homo sapi
C	22	133.4	5.4	246080	2	AC104073	AC104073 Homo sapi
C	23	133.2	5.4	168698	9	AC068138	AC068138 Homo sapi
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C	25	132	5.3	172724	2	AC098590	AC098590 Homo sapi
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C	27	131	5.3	130117	9	AC004907	AC004907 Homo sapi
C	28	131	5.3	158398	2	AC011146	AC011146 Homo sapi
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C	35	128.8	5.2	137889	9	AC073269	AC073269 Homo sapi
C	36	128.4	5.2	15421	3	PFCOMPIRA	X95275 P. falciparu
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C	38	127	5.1	101188	2	AC010606	AC010606 Homo sapi
C	39	127	5.1	184838	9	AC090740	AC090740 Homo sapi
C	40	126.8	5.1	152209	9	HS1108D11	AL034419 Human DNA
C	41	126.6	5.1	136098	9	AC006970	AC006970 Homo sapi
C	42	126.6	5.1	152209	9	HS1108D11	AL034419 Human DNA
C	43	126.4	5.1	246080	2	AC104073	AC104073 Homo sapi
C	44	126.2	5.1	135250	9	AC104320	AC104320 Homo sapi
C	45	126.2	5.1	136098	9	AC006970	AC006970 Homo sapi

ALIGNMENTS

PFMAL3P5 86827 bp DNA linear INV 04-MAY-2000  
Plasmodium falciparum MAL3P5, complete sequence  
AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162  
AL010206 AL010210 AL139179  
AL034556.3 GI:7711064  
HTG; centromere; CTRP protein; initiation factor E4;  
Serine/threonine protein phosphatase.  
Plasmodium falciparum  
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
1 (bases 1 to 86827)  
Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T.,  
Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T.,  
Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S.,  
Hornsby,T., Horrocks,P., Jagers,K., Jassal,B., Kyes,S., McLean,J.,  
Moule,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A.,  
Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S.,  
Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and  
Barrell,B.G.

RESULT 1  
PFMAL3P5/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result  
No. Score Match Length DB ID Description





SOURCE malaria parasite P. falciparum.  
ORGANISM Plasmodium falciparum  
REFERENCE Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
AUTHORS 1 (bases 1 to 67970)  
Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M.  
and Barrell,B.  
TITLE Direct Submission  
JOURNAL Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium,  
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge  
CB10 1SA, UK  
COMMENT On Dec 16, 1999 this sequence version replaced gi:5763807.  
For more information about this sequence or the Malaria Project,  
see [http://www.sanger.ac.uk/Projects/P\\_falciparum](http://www.sanger.ac.uk/Projects/P_falciparum). IMPORTANT: This  
sequence is unfinished and does not necessarily represent the  
correct sequence. Work on the sequence is in progress and the  
release of this data is based on the understanding that the  
sequence may change as work continues. The sequence may be  
contaminated with foreign sequence from E.coli, yeast, vector,  
phage etc.  
FEATURES  
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          /chromosome="1"  
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aa, similarity: upf0006 family eg to  
YBL055C/YBL0512/YBL0511, YBF5\_YEAST (418 aa), fasta  
scores: opt: 316, E(): 1.1e-12, (33.2% identity in 271 aa  
overlap)"  
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          /db\_xref="GI:6594244"  
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IIAKKEYEFTYKFNQOVNSKMGNGKICDGEKDMNNEILLEKNLDTIPGFY  
NEKKEYLENLKIILKYPNRIVCGIGELDFDLRLYSCSKYIQIKYFQLQVMPN  
LPMLHRNCSETFEKVIDIYKFLERNGVHFTDKEDIVHIIIVQNYKRLIGVNG  
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CDS  
misc\_feature  
misc\_feature  
gene

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YISFLKDFKVSGLVVMIFHLFEALHFLPHFLTINLKSVMFLYKINLCSSN  
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RALYHYIHMHKLDYEKLIQNEILLDKLIANNKISSYNNKSLVNYNFINEN  
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TLDNFLIEDILDVQVEYNIPEIQDKTLKYRGNTSEYMEKNLNLTIKESHGYSNLT  
IDYRIKLFDEVELNHNKSNKIYKAYFVKGTSEVSFSDINKEYIKMKKKNY  
KKEHNNKNNNNNNKDDHIYNMNDHNYANDINLGPNSTDODSDPSVSLGNE  
YLTDTYSSNSDKEIEVKPLYKDTHEFENKSSMPFKSSNNMNNNSFNKYENSS  
FKGISLETUWYFOQGVVLLTSVIFMLISIFTDEIKFVFTMMSIISKNKEHSD  
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/gene="MAL1P3.04"  
/note="MAL1P3.04, conserved hypothetical membrane protein,  
len: 203 aa, similarity: P. falciparum chromosome 2,  
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Query Match      5.8%; Score 144.4; DB 3; Length 67970;
Best Local Similarity 48.3%; Pred. No. 1.7e-10;
Matches 663; Conservative 0; Mismatches 681; Indels 30; Gaps 8;

QY 639 attaatggaggattattttccatataccaataatttttttttaatttcattgcatt 698
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DB 8389 AATATATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 8448
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QY 699 ttgatctattataaacaatttgatggattgaagtcgtatcggtgacaattgaag 758
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DB 8449 ATATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 8508
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QY 759 tttctcgaagtttagccattttttatgaattaaaccttaactactactattaggt 818
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DB 8509 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 8568
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QY 819 catatgataccaatttcgaatttcgaatttcgaatttcgaatttcgaatttcga 878
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DB 8569 AATATATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 8628
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QY 879 gtcaactctgttaactgaattgtattataaggttgacgacctttaacctaactc 938
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DB 8629 TAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 9762
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QY 939 tgaat-----tgaaggggttgatgactctcagcttttaataataattcaactaa 988
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DB 8689 AATATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 8748
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QY 989 ctgactcacattggagatttttaggttcataaaatttttagaaaaagctgagtt 1047
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DB 8749 TTAATAATATATAATAATAATAATAATAATAATAATAATAATAATAATAA 8808
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QY 1048 ---tatgaaaaaagattggtgactattccaatttaattgttggaattgatgaca 1103
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DB 8809 TTATATTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 8868
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QY 1104 tcatgacataccaatcagagaataaccacctgcgacgactacaacaatctc 1163
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DB 8869 AAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 8928
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QY 1164 ataaatgaagcattgtatagaagagctcagaataaattcttaataattagagg 1222
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DB 8929 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 8988
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DB 8989 AATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 9048
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QY 1283 ctaacaattttcttgactcacacattggttgatgggtgattttgtcacaata 1342
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DB 9049 ATATAATAATTTTAAATAATAATAATAATAATAATAATAATAATAATAA 9108
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QY 1343 tattttatactagtagattgtgtcgcgaattatatactagatttaactctgg 1402
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DB 9109 TATATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 9168
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QY 1403 tgcataataagttataaaaaaagga-----gaaaattattctcataaaa 1451
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DB 9169 ATATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 9228
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QY 1452 acacttaataagtaacaataataaaaaacattataaagagattaagataatt 1511
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DB 9229 ATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 9288
   || || || || || || || || || || || || || || || || || || || ||

QY 1512 -gtatgaagttagaataaattttttattataaaatttgaactaaataatt 1570
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DB 9289 TATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 9348
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QY 1571 caaagtaataatagataataattcatcatcaatcacgagtaattcaattat 1630
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DB 9349 TATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 9408
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QY 1631 tatattagataaataataca-aatatgttgtaaaattttacattattactacta 1689
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DB 9409 TAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 9468
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QY 1690 tattaatttttgaataatctttttatacaagtgaggtagacagagaattct 1749
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DB 9469 AAATTTACACATTTTAAATAATAATAATAATAATAATAATAATAATAA 9528
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QY 1750 ccgtattttgttagatgtaaaatgaacggcttagactgaatttttcttat 1809
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DB 9529 ATATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 9588
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QY 1810 tttaaatccattagagatttaagtttaagtctctct- ttgattttaaacatg 1868
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DB 9589 TTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 9648
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QY 1869 aattaggtttaatcatcattgogtccatgaacccatgctatattgtttta 1928
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DB 9649 TAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 9708
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QY 1929 tttttgacaagtgttttttttttttttttttttttttttttttttttttt 1982
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DB 9709 ATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 9762
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RESULT 3
AC093899 172816 bp DNA linear PRI 05-FEB-2002
LOCUS Homo sapiens chromosome 2 clone RP11-724016, complete sequence.
AC093899 AC068884
AC093899.3 GI:18497265
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE
1 (bases 1 to 172816)
AUTHORS
Waterston,R.H.
JOURNAL
The sequence of Homo sapiens clone
Unpublished
REFERENCE
2 (bases 1 to 172816)
AUTHORS
Waterston,R.H.
JOURNAL
Direct Submission
Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE
3 (bases 1 to 172816)
AUTHORS
Waterston,R.H.
JOURNAL
Direct Submission
Submitted (05-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT
On Feb 5, 2002 this sequence version replaced gi:15625013.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: H_NH0724016
Drafting center: WIBR
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FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-724016"
BASE COUNT 53405 a 33788 c 33104 g 52519 t
ORIGIN
Query Match 5.8%; Score 144.4; DB 9; Length 172816;
Best Local Similarity 47.7%; Pred. No. 1.3e-10;
Matches 653; Conservative 0; Mismatches 696; Indels 21; Gaps 7;
QY 628 ttctactctttaaaggaggattttttccatataccaatttaattttttta 687
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DB 22801 TTTAATAATATTTATATAAATATATTTTATATAAATATATATTTAATAATAATATCTT 22860
QY 688 atttatgaatttgatcttatataaacaattatggtatgattgaatcgatatacggt 747
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DB 22861 TATATTTAATATATTTAATAATAAATATCTTTATATTTAATATATATTTATATAAAT 22920
QY 748 gcaattgaagtttccccaagtttagccatttttatgaaaataaactaacactacta 807
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DB 22921 -ATATATTTAATTTAATAATATTTAATTTAATAATACGGTTATTTAATAATATATTTT 22979
QY 808 tttaggttaattcatatgatcattacaatttcaattgagttcatttttaaccagaagt 867
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DB 22980 CTAATAAATATATTTATATAACATATATTTATATAAATATATTTATATATTTAATAATA 23039
QY 868 tgaagttgttgcaactctctgttaactaaagtgttatataaagggtgacgacttaacc 927
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DB 23040 TTTACATATAAATATATTTATATGTAATATATTTACATATAAATATATTTATATTTAATA 23099

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QY 928 taaatctatttgaattgaagggttgatgacttcagctttaaataaataaactcaactaaagt 987
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DB 23100 TATATGCATATGTAATAATATATTTATTTATTAATAATAATAATAATAATAATAATAATA 23159
QY 988 tctagactacattggagagatttttagtgcataaaaaatttttagaaaaaggctgagtttaaagt 1047
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DB 23160 TAAATAATATTTATATAATAATATATTTATTTAATAATAATAATAATAATAATAATAATA 23219
QY 1048 tatgaaaaa--gattggtagctattccaatttaatttggttgtaattgtagacaaatatttc 1105
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DB 23220 TAAATATATTAATAATATTTAATAATAATAATAATAATAATAATAATAATAATAATAATA 23279
QY 1106 atgagcaacaacaatcacagagaataaccacctcgccgactcaacaactcctaattgaat 1165
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DB 23280 TTTATATTTAATAATAATAATAATAATAAACAATAATAATAATAATAATAATAATAATA 23339
QY 1166 taatgaagcattgtagtaaggagctctagaataaattctttaaataatttagaggaaaact 1225
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DB 23340 AACATATATTTATATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 23399
QY 1226 atttttaaaaaat-----tacaagaaaagtttgatcctataaacctctttaaactttaaatt 1280
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DB 23400 ATATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 23459
QY 1281 atctaacaattttctctatgactcacatctggttgtagagggtgattttgtcaaaatatatg 1340
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DB 23460 ATATATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 23519
QY 1341 tctattttatactagctatgattgtctgcgaattatatactatgatttaactgtggagaaatg 1400
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DB 23520 TTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 23579
QY 1401 attgctctaataagttcataaaaaaggagaaaatactatttctcataaaaaatacaccttaaa 1460
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DB 23580 TTT--ATATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 23637
QY 1461 laagcaacaataaataaaacettatataaagagatcaagataaatttaactgaattcattgaat 1520
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DB 23638 TATTTATATTTAATAATAACATATAATAATAATAATAATAATAATAATAATAATAATAAT 23697
QY 1521 gtagaataatttttataaattgaacta-aaattccaataaataattcacaagtaaa 1579
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DB 23698 TAAATATACATATATATTTATTTAATAATAATAATAATAATAATAATAATAATAATAAAT 23757
QY 1580 taatagatataattcattcaataacgagtaattcaactcattataatcaatcatatattaga 1639
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DB 23758 ATATATTTATATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATG 23817
QY 1640 taaatatacaaatatttgttaaaattttacattattatactaaataataataatttc 1699
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 23818 AATATATACATAAAT------ATATATTTATTTAATAATAATAATAATAATAATAATAAT 23870
QY 1700 ttgtaatatctttatacaagtaggtagactagagaatactctctatcccgatattt 1759
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 23871 TATATATTTAATAATATTTATTTAATAATAATAATAATAATAATAATAATAATAATAATAAT 23930
QY 1760 gtatagtgtaa---atgtaacgggttagactgagttttgttattattattattataaaa 1816
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DB 23931 ATATATACATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 23990
QY 1817 tccattgagatttaagttaactgctctctcttggatttttaaacatggttctcaaaaattaggt 1876
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 23991 ATTTATGTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 24050
QY 1877 ttaactatgcgcctcaatgaacccatgctatgattgttttaaagttttttgtttttgac 1936
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 24051 ATATTTATATATTTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAAT 24110
QY 1937 aatgttttttattctctgagagtgctcttaggactgaaactatctgtttgata 1986
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 24111 ATATTTATATATATATATTTTATATATAATAATAATAATAATAATAATAATAATAATAATA 24160

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RESULT	4
DMU11584/c	
LOCUS	Drosophila melanogaster Oregon-R mitochondrial A+T region.
DEFINITION	4601 bp DNA linear INV 23-JUL-1994
ACCESSION	U11584
VERSION	U11584.1 GI:508826
KEYWORDS	mitochondrial DNA; A+T region; tandem repeats.
SOURCE	fruit fly.
ORGANISM	Mitochondrion Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 4601) Lewis,D.B., Farr,C.L., Farquhar,A.L. and Kaguni,L.S. Sequence, Organization and Evolution of the A+T Region of Drosophila melanogaster Mitochondrial DNA Mol. Biol. Evol. 11, 523-538 (1994)
REFERENCE	2 (bases 1 to 4601) Kaguni,L.S. Ission Direct Submission Submitted (28-JUN-1994) Laurie S. Kaguni Ph.D, Dept. of Biochemistry, Michigan State University, East Lansing, MI, 48824-1318, USA
FEATURES	Location/Qualifiers 1..4601 /organism="Drosophila melanogaster" /organelle="mitochondrion" /strain="Oregon-R" /db_xref="taxon:7227" /dev_stage="embryo" 650..1022 /note="repeat I-A" /rpt_type=tandem 1023..1360 /note="repeat I-B1" /rpt_type=tandem 1361..1705 /note="repeat I-C/A" /rpt_type=tandem 1706..2043 /note="repeat I-B2" /rpt_type=tandem 2044..2388 /note="repeat I-C" /rpt_type=tandem 2491..2511 /note="deoxythymidylate stretch" 2512..2648 /partial /rpt_type=tandem 2649..3112 /note="repeat II-A" /rpt_type=tandem 3113..3576 /note="repeat II-B1" /rpt_type=tandem 3577..4040 /note="repeat II-B2" /rpt_type=tandem 4041..4504 /note="repeat II-C" /rpt_type=tandem misc_feature complement(4565..4585) /note="deoxythymidylate stretch"
BASE COUNT	2271 a 131 c 74 g 2125 t
ORIGIN	
Query Match	5.88; Score 143.6; DB 3; Length 4601;
Best Local Similarity	45.7%; Pred. No. 4.8e-10;
Matches 662; Conservative	0; Mismatches 774; Indels 14; Gaps 4;

[illegible]

Query Match 5.8%; Score 143.6; DB 3; Length 4601;  
Best Local Similarity 45.7%; Pred. NO. 4.8e-10;  
Matches 562; Conservative 0; Mismatches 774; Indels 14; Gaps 4;



tRNA	3012...3077 /product="tRNA-Leu"
CDS	3083...3767 /note="TAA stop codon is completed by the addition of 3' A residues to the mRNA" /codon_start=1 /transl_except=(pos:3767,aa:TERM) /transl_table=5 /product="cytochrome c oxidase subunit II" /protein_id="AAC47813.1" /db_xref="GI:1166532" /translation="MSTWANLGLQDSASPLMEQLIEFPHDHALLILVMTIVLVGYLMFM LFFNVRFLRGLQLEMIWTLLPALILLFIALPSRLRLYLDEINEPSTVLKSI GH QWYSEYSDFNNTEDFSYMPTNELMDGFRLLDVRNLPMNSQIRILVTAADVI HSWTPALGVKVDGTGRCLNQTNFFINRPGIFYCQCSEICGANHSPMPDIVESVPVNY FIKWTSSNN\$" 3768...3838 /product="tRNA-Lys" 3840...3906 /product="tRNA-Asp" 3907...4068 /codon_start=1 /transl_table=5 /product="ATPase 8" /protein_id="AAC47814.1" /db_xref="GI:1166533" /translation="MPQMAPI\$MLLFIFISITFILFC\$INYYSMPNPK\$KSELKNKI NLNSNNKW\$" 4062...4736 /codon_start=1 /transl_table=5 /product="ATPase 6" /protein_id="AAC47815.1" /db_xref="GI:1166534" /translation="MMNLNSHPDPLAFNFSLNWLSTFLGLMWIPSIYWLMP\$RYNI MNSILLTLHKFEYTLGLPGSHNGSTFI\$LSLILFNFMGLFPFYFTSTSHLIT LSLAQLWCFLMYGNWHNTOHMF\$AHLVPOGTFAILMPFVCITETSNIIIRPGTLAVR LTANNIAGHLLLTLLIGNTGSSMSYMLM\$TFLIMAQIALLVLESAMVIO\$SYVFAVL\$TL YSEVN\$" 4736...5524 /codon_start=1 /transl_table=5 /product="cytochrome c oxidase subunit III" /protein_id="AAC47816.1" /db_xref="GI:1166535" /translation="M\$THSNHPFLVDY\$PWPLTGATGAMTVSGMKVPHOYDISLF VLGNITLITYQWRDV\$REGTYOGLHYAVTIGLWGMLILFELSEYLFYVSFFWAF FHSSLSPAIELGASWPNGIISFPFQPPLNTAILLASGVTVYWAH\$LSMNHN\$QT TOGLFVLLGIYTILOAYEYIEAPTIADSIYGTSFFMATFGHHIVHLIGLITFFLL CLLRHLNH\$FKNHGFGEAAA\$WHEFVDVWVLFLYITIYWGG\$" 5543...5607 /product="tRNA-Gly" 5608...5961 /codon_start=1 /transl_table=5 /product="NADH dehydrogenase subunit 3" /protein_id="AAC47817.1" /db_xref="GI:1166536" /translation="M\$SIIIFIATLILITIVMPELASILSKKALIDREK\$SPCECFGD PKSSRLPF\$URFFLITIFLDFVEIALILPMIIMKY\$NMIMTWITITSIFILILI GLYHEWNOGMLNWSN\$" 5981...6045 /product="tRNA-Ala" 6055...6118 /product="tRNA-Arg" 6119...6183 /product="tRNA-Asn"
tRNA	
tRNA	
tRNA	

tRNA	6184. .6251
/product="tRNA-Ser"	
tRNA	6252. .6318
/product="tRNA-Glu"	
tRNA	complement(6337..6401)
/product="tRNA-Phe"	
CDS	complement(6401..8124)
/note="TAA stop codon is completed by the addition of 3' A residue to the mRNA"	
/codon_start=1	
/transl_except=(pos:complement(6401..6402),aa:TERM)	

  

Query Match	5.8%; Score 143.6; DB 3; Length 19517;
Best Local Similarity	45.7%; Pred. No. 3.2e-10;
Matches	662; Conservative 0; Mismatches 774; Indels 14; Gaps

  

Qy	665	tataccaattaatttttaattatgcattttgatcttatcatacaacaatttg	724
Db	18471	TTTTAAAAATTTATTATAAATTTTAAATAATTTTAATTTTCATATATATATATAT	18412
Qy	725	tatggattaaagtcgtacggtgcacattgaagtgttcccgacttagcattttat	784
Db	18411	TATATAATATTCATTAATATATAAATTTTAAATATATATAATTAATTAATTAATCACTAT	18352
Qy	785	gaattaaactaacactactacttagttaactcatatgatcatcaacaatttcaatg	844
Db	18351	ATTATTATATAAATTTAAATTAATAA--TAAATAAATAGAGAATAAATTTTATATAA	18294
Qy	845	tgagtcaaattttaccocaagattggaagtttgtgtcaacctctgttaactaaagttgta	904
Db	18293	TTATATCTACATTTTAAATTTTAAATTTTATTTAAATTTATAGATATATAATATA	18234
Qy	905	ttataaggtgacgactttaaccctaactattttgaattgaagggtgtgatgacttcag	964
Db	18233	TATTAAATATTTATATATATAAATAATCTATTAATTTTAAATTAATTAATGATATAGT	18174
Qy	965	ctttaaaaataactcaactaaagttctagacatctggagatttttagtggctcaaaaatt	1024
Db	18173	TTAAAAAAAATTTATTTTAAAAATTTTAAAAATTTTAAAAATTTGAAAAATATAAT	18114
Qy	1025	ttagaanaagctgagttaaagttatgaaaaagattggctacttccaattcaattagttg	1084
Db	18113	ATATTTCATTATAAAATTTATTTTATAAAATTTTGTGTTTATTTTAAAAAACATCAT	18054
Qy	1085	tgaattgatgacaaatatctcatgacataaccaatcacagagaaataccaccctgcacgac	1144
Db	18053	TTTATATATAAATATTTTATAAAAATATACATTTAAGAAAT-----TTTTAAAAA	17999
Qy	1145	tacaacaatccaatgttaattaatgaagcattgtagataaaggagctagaataaattt	1204
Db	17998	TTTATATTAATTTATTTAAATTTTAAATTTTCTATATATATATATATATATAAAT	17939
Qy	1205	ottaaaaattagaggaanaaactattttaaaaaattacaagaaagtttgatctataacct	1264
Db	17938	ATTCAATAATATAAANA----TTTATAAATATATAAATAAATTAATTAATTTATTATTAT	17883
Qy	1265	cttlaaacttttaaattatctcaactttcttatgactccacattgtgtgtgataagggtgat	1324
Db	17882	TTATATAAATTTAAATTAATAAATAAATAATATGAATATAAATTTTATTAATTTATATC	17823
Qy	1325	tttgtcaaaaatatgtctattttatactagtagattgtctgcgaattatataagta	1384
Db	17822	TACATTTTAAATTTTAAAAATTTTATTTAAATTTTATAGATATATAATATAATTAATA	17763
Qy	1385	ttaaactggagaataatgctgctaataagtttataaaaaaggagaaaaattattatcataa	1444
Db	17762	TATTATATATATATAAATATCTATTAATTTATAATTAATTAGTATATAGTTTTTTTAAAA	17703
Qy	1445	aaaaaatcacacttaataagtaacaaataaaaaaacattataaagagattaagataat	1504
Db	17702	AAAAATTTTTTTTAAAAAATTTTTTTTTTAAAAATGAAAAATTAATTAATTTATATATTC	17643
Qy	1505	ttaataagattggaatgtagaataatttttattataaattttgactaaaaatatctcaaat	1564

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Db 17642 ATTATAAAATTTATTATTAAAAATTTTGTGTTTATTTTAAAAACATGATTTTATTA 17583
Qy 1565 aatattcaagtaagaatagatatataatcattcatcattcaatcagtagtaattcaatctatta 1624
Db 17582 TATAAATATTTTATAAAAAATACACATTTAAGAAATTTTAAAAAATTTTATATTAAT 17523
Qy 1625 taatcatatattagataaatacacaaatattgttcaaatctttacattattattactaa 1684
Db 17522 TATTTAATAATTTAATTTTCTATATATATATATATATATATTAATATTCATATATAT 17463
Qy 1685 atatatataatcttttgatataatctttttacaaagtaggtagactagaagaattcttt 1744
Db 17462 AAATTTATAAATATATAAATTAATTAATTTAATTTAATTTAATTTAATTTAATTTAAT 17403
Qy 1745 atctcccgatatattgtagatgttaaatgttaacgggcttagactgagatcttttctattat 1804
Db 17402 TTTTATTATTAAATTAATTAATTTAGTAATTAATTAATTTTATTAATTTAGTTATTAAA 17343
Qy 1805 attattataaaccattagagatttaagttaagtctctctctctctctctctctctctctc 1864
Db 17342 TTTATTTATTATTAAATTAATTAATTAATTAATTAATTAATTAATTTTATTAATTTAAT 17286
Qy 1865 taasaatcagggtttaatcattcgctccctcaatgaaccccatgctatatgttttaagtttt 1924
Db 17285 TTAATTTATTATTATTATAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAAT 17226
Qy 1925 tctgtttttgacaatgttttttttattcttgagattgctctcttaggactgaaattatgttga 1984
Db 17225 ATATATATAAATTTTATTAAATTTTAAATTAATTTTAAATTAATTTTAAATTAATTA 17166
Qy 1985 tactagaaaaacgaagtagagagtagtgatatacacacgtgttaaaaaataaatagttgtgg 2044
Db 17165 AAATAGTTTATTAAAGTATAAATTTAATAAATAATTTTAAATTTTAAATTTTAAATTT 17106
Qy 2045 aacttaagttggatttgaaactaggacgagcgctggaggggtttccactaagttgacaaa 2104
Db 17105 AGTTTAAATTAATAAATAAATTTATGAATAGGGGAATAAATTTATTTTCATTTTACATA 17046
Qy 2105 aattattaca 2114
Db 17045 TATATATATA 17036

RESULT 6
AC096750/c
LOCUS AC096750 Homo sapiens chromosome 4 clone RP11-426F15, complete sequence.
DEFINITION AC096750 AC086867
ACCESSION AC096750.3 GI:16418260
VERSION AC096750.3 GI:16418260
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 159618)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159618)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 3 (bases 1 to 159618)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Oct 25, 2001 this sequence version replaced gi:16259145.
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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: H_NH0426F15
Drafting center: WIBR
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FEATURES             Location/Qualifiers
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                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="4"
                        /clone="RP11-426F15"
BASE COUNT           51014 a 29807 c 29529 g 49268 t
ORIGIN
Query Match          5.8%; Score 142.6; DB 9; Length 159618;
Best Local Similarity 46.8%; Pred. No. 2.3e-10;
Matches 671; Conservative 0; Mismatches 739; Indels 25; Gaps 6;
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DEFINITION		Homo sapiens chromosome 4 clone RP11-324J13, WORKING DRAFT	
ACCESSION		AC098590.2	GI:16596634
VERSION		HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.	
KEYWORDS		human.	
SOURCE		Homo sapiens	
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REFERENCE		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 172724)	
TITLE		Waterston, R.H.	
JOURNAL		The sequence of Homo sapiens clone	
REFERENCE		Unpublished	
AUTHORS		2 (bases 1 to 172724)	
TITLE		Waterston, R.H.	
JOURNAL		Direct Submission	
COMMENT		Submitted (25-OCT-2001) Genome Sequencing Center, Washington	
		University School of Medicine, 4444 Forest Park Parkway, St. Louis,	
		MO 63108, USA	
		On Nov 2, 2001 this sequence version replaced gi:16418249.	
		----- Genome Center -----	
		Center: Washington University Genome Sequencing Center	





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DEFINITION			
ACCESSION			
VERSION			
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Qy	1493	gattaagaataatttaataagattggaatgagaataattttttattatacaattigaacta 1552

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

#### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3 6

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-314B1, 2000 bp overlap; the clone sequenced to the right is RP11-86017. Actual start of this clone is at base position 161288 of RP11-314B1; actual end is at base position 168698 of RP11-813K12.

Data from AC069383 was used to finish this clone, AC068138. An unresolved di-trinucleotide repeat exists between 52436 and 52756.

#### FEATURES

source

Location/Qualifiers

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DEFINITION Sequence 6 from Patent WO0200932.					
ACCESSION AX344555					
VERSION AX344555.1 GI:18492441					
KEYWORDS synthetic construct.					
SOURCE synthetic construct					
ORGANISM artificial sequence.					
REFERENCE 1 (sites)					
AUTHORS Olek.A., Piepenbrock,C. and Berlin,X.					
TITLE Diagnosis of known genetic parameters within the mhC					
JOURNAL Patent: WO 0200932-A 6 03-JAN-2002;					
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Matches 616; Conservative 0; Mismatches 659; Indels 24; Gaps 6;

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DEFINITION  
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\*\*\*, 3 unordered pieces.  
AC005504  
AC005504.3 GI:4558584  
VERSION

AC005504  
Plasmodium falciparum chromosome 12, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*, 3 unordered pieces.  
AC005504  
AC005504.3 GI:4558584  
VERSION







JOURNAL REFERENCE	Unpublished	QY	1271	actttaaattatatacaaaattttcttatgactcacacattgtgttgataggggtgattttgtc	1330
AUTHORS	Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.				
TITLE	Direct Submission	Db	73825	ATGGTTATTTTATTTTAAATTTAAATGTGA--AATATATTATTATTATATTAATAAAAAA	73882
JOURNAL	Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA	QY	1331	aaaatatatgctctattttatactactagtagtatgatttgcgcgaattacatatagattcaact	1390
COMMENT	On Apr 2, 1999 this sequence version replaced gl:4337172. * NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * 1 58642: contig of 58642 bp in length * 58643 58842: gap of unknown length * 58843 91011: contig of 32169 bp in length * 91012 91211: gap of unknown length * 91212 104992: contig of 13781 bp in length.	Db	73883	TATATATATATTTTAAATTAATTAATATATGTTTATATATTTTAAATTTAAATATATATTT	73942
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		QY	1451	tacacttaaatgaagtaacaataaaaaaacattataagaagattgaagaattttaata	1510
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		QY	1810	ttataaattccattagaggatttaagttaagtctctctctctgttttgaacttggtctcaaa	1869
		Db	74361	TATTAATTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATAA	74420
		QY	1870	attcaggtttaaattcattcgctcccaatgaaccatgctatatttgaaggtttttgtt	1929
		Db	74421	TTTTAATAATGAATTTATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTA	74480
		QY	1930	ttttgacaatgtttttttattctctgagatgctctta	1965
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Search completed: August 21, 2002, 02:28:10  
Job time: 11106 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 23:27:59 ; Search time 477.34 Seconds  
(without alignments)  
6916.719 Million cell updates/sec

Title: US-09-763-957-1

Perfect score: 1923

Sequence: 1 atctctctccacttactt.....aggtcttcaattcatttc 1923

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	735	38.2	1888	19	AAV31482	Papaya ACC synthas
4	691.6	36.0	1868	18	AAV73502	Poplar 1-aminocycl
5	686.4	35.7	1878	19	AAV30326	Pelargonium 1-amin
6	672.8	35.0	2088	19	AAV20947	Coffee-fruit speci
7	635.2	33.0	1113	18	AAV72632	Mangifera indica A
8	630.2	32.8	1775	12	AAQ15134	Clone ptACC1 encod
9	630.2	32.8	1818	22	AAQ04546	Tomato 1-aminocycl

10	630.2	32.8	2230	19	AAV15704	Tomato ACC synthas
11	630.2	32.8	2230	22	AAQ04544	Tomato 1-aminocycl
12	630.2	32.8	2230	22	AAQ23621	Tomato ACC synthas
13	627	32.6	1800	19	AAV09713	ACC synthase DNA.
14	627	32.6	2678	19	AAV30325	Pelargonium 1-amin
15	625.4	32.5	1934	18	AAV66246	ACC synthase GAC-1
16	625.4	32.5	1945	19	AAV30324	Pelargonium 1-amin
17	623.2	32.4	1170	18	AAV66247	ACC synthase GAC-2
18	607.2	31.6	1780	12	AAQ15138	Clone ptACC5 encod
19	607.2	31.6	1781	12	AAQ15137	Clone ptACC4 encod
20	607.2	31.6	1783	12	AAQ15136	Clone ptACC3 encod
21	607.2	31.6	1793	12	AAQ15139	Clone ptACC6 encod
22	607.2	31.6	1818	12	AAQ15135	Clone ptACC2 encod
23	582.4	30.3	1703	12	AAQ15131	Clone ptACC1 encod
24	582.4	30.3	1703	19	AAV15701	zucchini ACC synth
25	582.4	30.3	1703	22	AAQ04541	zucchini 1-aminocy
26	582.4	30.3	1703	22	AAV23618	zucchini ACC synth
27	574.6	29.9	1942	13	AAV38896	Carnation ACC synt
28	572.8	29.8	1482	13	AAQ25896	ACC synthetase gen
29	571.4	29.7	1712	20	AAV27501	Banana 1-aminocycl
30	571.4	29.7	1712	22	AAQ09901	DNA encoding 1-ami
31	571.2	29.7	1104	18	AAV72629	Carica papaya ACC
32	567.8	29.5	1096	18	AAV72631	Mangifera indica A
33	532.8	27.7	15397	18	AAV58635	T-DNA insert of 13
34	531.2	27.6	15397	18	AAV58635	Carnation ACC synt
35	494.8	25.7	1087	17	AAV38897	Carica papaya ACC
36	466.8	24.3	1098	18	AAV72630	Ananas comosus ACC
37	464	24.1	1080	18	AAV72628	Tomato ACC synthas
38	408.6	21.2	7244	19	AAV15705	Tomato 1-aminocycl
39	408.6	21.2	7244	22	AAQ04545	Tomato ACC synthas
40	408.6	21.2	7244	22	AAV23622	Tomato ACC synthas
41	407.6	21.2	7241	12	AAQ15140	Genomic clone LE-A
42	361.4	18.8	5613	15	AAQ63241	Crucifer 1-aminocy
43	307.2	16.0	968	19	AAV00219	1-aminocyclopropan
44	299.4	15.6	993	17	AAV33139	Broccoli ACC synth
45	276	14.4	7587	19	AAV15703	zucchini ACC synth

ALIGNMENTS

RESULT 1  
ID AZ94267  
ID AZ94267 standard; cDNA; 1923 BP.

XX AC AZ94267;

XX DT 03-JUL-2000 (first entry)

XX DE Mung bean ACC synthase AIM-1 cDNA.

XX KW Mung bean; 1-aminocyclopropane-1-carboxylic acid synthase;  
XX KW ACC synthase; AIM-1; promoter; pGEL-1; transgenic plant; ss.

XX OS Vigna radiata.

XX FH Key Location/Qualifiers  
XX CDS 88..1542

XX FT /\*tag= a

XX PN WO200012714-A1.

XX PD 09-MAR-2000.

XX PF 31-AUG-1999; 99WO-AU00705.

XX PR 31-AUG-1998; 98AU-0005572.

XX PA (UYQU ) UNIV QUEENSLAND.

XX PI Botella Mesa JR, Cazzonelli CI;

XX XX WPI; 2000-270821/23.

P-PSDB; AAY79292.

Isolated nucleic acid molecule for producing transgenic plants having altered characteristics such as resistance to a plant pathogen comprises promoter, inducible in response to physical stimulation - Claim 41; Page 98-101; 11pp; English.

The present sequence is that of cDNA encoding mung bean 1-aminocyclopropane-1-carboxylic acid synthase (ACC synthase, see AA97992). The ACC synthase gene, AIM-1, is induced in response to mechanical strain, auxin and salt stresses. The invention relates to the pGEL-1 promoter (see AA294266) that directs expression of the AIM-1 gene. pGEL-1 is capable of induction by physical and/or environmental stimuli in cells in which it is indigenous and, in the absence of any negative regulatory mechanism, is capable of constitutive expression in cells in which it is non-indigenous. The promoter can be used to direct expression of genes conferring useful traits on plants, such as improved resistance to a plant pathogen, altered nutritional characteristics, expression of a plantabody, altered biochemical pathway, altered fertility, and/or altered flower colour.

Sequence 1923 BP; 548 A; 383 C; 426 G; 566 T; 0 other;

Query Match	100.0%;	Score 1923;	DB 21;	Length 1923;
Best Local Similarity	100.0%;	pred. No. 0;		

0:

Qy	1	atcctctctcccacttactctgatttcaatccaaataaactcaacacactttttac	60
Db	1	atcctctctcccacttactctgatttcaatccaaataaactcaacacactttttac	60
Qy	61	actccacactctaaccacatacaccatactgggtttcaaggccatgacacaaactccctg	120
Db	61	actccacactctaaccacatacaccatactgggtttcaaggccatgacacaaactccctg	120
Qy	121	ttgtccaaagtggctattggggatggacatggcgaaatccccatactttgatggatgg	180
Db	121	ttgtccaaagtggctattggggatggacatggcgaaatccccatactttgatggatgg	180
Qy	181	aaggcttatgatcaaaaccccttccatccccacagataactcctaagcgtgttatgcaaatg	240
Db	181	aaggcttatgatcaaaaccccttccatccccacagataactcctaagcgtgttatgcaaatg	240
Qy	241	ggctctgtcgagaatcagcttaactctgatttggtagagattgggatactgaacaacct	300
Db	241	ggctctgtcgagaatcagcttaactctgatttggtagagattgggatactgaacaacct	300
Qy	301	gaagcctccatttgcactccagaagaataaatgatttcaggggccatagctaactttcag	360
Db	301	gaagcctccatttgcactccagaagaataaatgatttcaggggccatagctaactttcag	360
Qy	361	gattatcatgcttggccgagttccagaaatctgctggctcaaatattatgcttagaacaagg	420
Db	361	gattatcatgcttggccgagttccagaaatctgctggctcaaatattatgcttagaacaagg	420
Qy	421	ggaaacagaatacagtttgacctgaccgtattgtcatgagcgtggagccaccggagca	480
Db	421	ggaaacagaatacagtttgacctgaccgtattgtcatgagcgtggagccaccggagca	480
Qy	481	cacgaagtcaactgcctttgtttggcagatcccgcgagcattcttagtgccattccc	540
Db	481	cacgaagtcaactgcctttgtttggcagatcccgcgagcattcttagtgccattccc	540
Qy	541	tattatccaggcctttgaccgggatttgaggtggagacacaggagtttaaaactgttcagtt	600
Db	541	tattatccaggcctttgaccgggatttgaggtggagacacaggagtttaaaactgttcagtt	600
Qy	601	atgtgcgatagtcacaataattctgatttgacaaagggaagcaatttgaagatgcctatgag	660
Db	601	atgtgcgatagtcacaataattctgatttgacaaagggaagcaatttgaagatgcctatgag	660

Qy	661	aaagcaagagaggataacatcagagtaaaaggtttactgatcaccaatccatcaaatcca	720
Db	661	aaagcaagagaggataacatcagagtaaaaggtttactgatcaccaatccatcaaatcca	720
Qy	721	ttagcgacaatcatggacagaaagacactgagaaccgtagtgagcttcaatcgaagaag	780
Db	721	ttagcgacaaatcatggacagaaagacactgagaaccgtagtgagcttcaatcgaagaag	780
Qy	781	cgatccacccttgatgtgataaataatgctgcgaacagttttcagccaaacccggttcc	840
Db	781	cgatccacccttgatgtgatgaataataatgctgcgaacagttttcagccaaacccggttcc	840
Qy	841	ataagcatagctgagatattagaggatgaacaacagacatagatgtagccgcaacctccta	900
Db	841	ataagcatagctgagatattagaggatgaacaacagacatagatgtagccgcaacctccta	900
Qy	901	cacattgtttatagctcttcaaaaggacatgggttccctggcttcagatcgagcatcata	960
Db	901	cacattgtttatagctcttcaaaaggacatgggttccctggcttcagatcgagcatcata	960
Qy	961	tactettacaatgatctgtgtgttaatttggcagcgaataatgcgaagctttggattggtg	1020
Db	961	tactettacaatgatctgtgtgttaatttggcagcgaataatgcgaagctttggattggtg	1020
Qy	1021	ccaacacagactcagtatcttttagcatcgatgctaaatgatgatgattgttgagagg	1080
Db	1021	ccaacacagactcagtatcttttagcatcgatgctaaatgatgatgattgttgagagg	1080
Qy	1081	ttctggcagagagtgcgaagaggttggctcaaaagcttcaaggttttcaactgggggttg	1140
Db	1081	ttctggcagagagtgcgaagaggttggctcaaaagcttcaaggttttcaactgggggttg	1140
Qy	1141	gccaaagtggcataaagtcttgcgaagcaatgctggtctatttgtgtgtagatttta	1200
Db	1141	gccaaagtggcataaagtcttgcgaagcaatgctggtctatttgtgtgtagatttta	1200
Qy	1201	aggcaactctcaaaaagccaactctgcactctgaacaggagctttggaagattatcatt	1260
Db	1201	aggcaactctcaaaaagccaactctgcactctgaacaggagctttggaagattatcatt	1260
Qy	1261	catgaagttaagatcaatgtttcaactggctattctctccattgcacgagccagggctgg	1320
Db	1261	catgaagttaagatcaatgtttcaactggctattctctccattgcacgagccagggctgg	1320
Qy	1321	tttagggctgctatgccaaactcggatgatattgctgtgcgaatgctttgcacagcaatc	1380
Db	1321	tttagggctgctatgccaaactcggatgatattgctgtgcgaatgctttgcacagcaatc	1380
Qy	1381	cgaactttgtcttcaaaacaaaggggtcggtgtgtctaaatgaagaacattgttggcac	1440
Db	1381	cgaactttgtcttcaaaacaaaggggtcggtgtgtctaaatgaagaacattgttggcac	1440
Qy	1441	agtaacttgaggtcgacctcaaaaacagaggttgcatacaccatgctaccttcac	1500
Db	1441	agtaacttgaggtcgacctcaaaaacagaggttgcatacaccatgctaccttcac	1500
Qy	1501	tctccctacactcagtcacctaattgttaagccaaataatggatttgcatactctctga	1560
Db	1501	tctccctacactcagtcacctaattgttaagccaaataatggatttgcatactctctga	1560
Qy	1561	atcggttagaagaagtaactgatgatggaattacttggttcttttattgtatttttg	1620
Db	1561	atcggttagaagaagtaactgatgatggaattacttggttcttttattgtatttttg	1620
Qy	1621	agaaggtacataaagtgcgtgattgttcttttgggaacagcaataacaggaataatcctgatg	1680
Db	1621	agaaggtacataaagtgcgtgattgttcttttgggaacagcaataacaggaataatcctgatg	1680
Qy	1681	ttggtttgtagatcgggaatacaataacagtgctcctacaaagtgtgctgtctcatgcaagcc	1740
Db	1681	ttggtttgtagatcgggaatacaataacagtgctcctacaaagtgtgctgtctcatgcaagcc	1740





Db 942 tatcttcgcaaacccagtagtctatgtagcatccatgtagcagacgtagaattgtgagacc 1001  
 QY 1079 ggtttctggcagagagtgcaaaagagtggtgctcaaaaggttcagggttttctactgggggt 1138  
 Db 1002 aattttatgtagagagcagaagaggtggtgcaatgagacatagtttttccacaaaagac 1061  
 QY 1139 tggccaaagtgtgcataaaagtgttcgcaaaagcaatgctggtctatcttgtgtgtaggatt 1198  
 Db 1062 ttgctcaagtaggcattaaactgttttaaaagcaatgctggtcttcttgtgtgtaggatt 1121  
 QY 1199 taaggcaacttctcaaaaagccaaacttgcactctgaacggagcttttgaaagtattaca 1258  
 Db 1122 tgcgtagactgctgaaagaacagacacatttgaagcagaaaatggtgtatggagagtaatta 1181  
 QY 1259 ttcataagtgtaagatcaaatgtttcaacctggtctattctctccattgcactgagccagggt 1318  
 Db 1182 taacagaaaataaaactcaatgtatctctggttgcgtcttctccactgctcgaacccgtgct 1241  
 QY 1319 ggtttagggtgtgctatgccaacatggatgatagctgtgctgcaaatgctttgcaacgaa 1378  
 Db 1242 ggttcgggggttctgttgcaaacatggagcagataagacaaatggaaatgcaactgcaagaa 1301  
 QY 1379 tccgcaacttgtgctcacaacaaagaggtcgtggtgtctataaagaacacattgttggc 1438  
 Db 1302 tcaaaaccttcagcttcaacataagaagcaaatggtgcctaaagaacacattgttggc 1361  
 QY 1439 acagtaacttgaggtgagcctc-----aaaccagaaggtttgatgata 1483  
 Db 1362 aaactagcttagactcagcttctctctcgtctgctatgaggatcatcaggtgagacacccgggt 1421  
 QY 1484 tcaccatgcactcactcctccctcactcagtcacgtcactcagtcactatggttaagcca 1534  
 Db 1422 cgttcagctctcactcagctcctatacctcaatcactcttctgttgagcca 1472

## RESULT 4

AAT73502  
 ID AAT73502 standard; cDNA to mRNA; 1868 BP.  
 XX  
 AC AAT73502;  
 XX  
 DT 26-AUG-1997 (first entry)  
 XX  
 DE Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS2.  
 XX  
 KW Ozone; induction; exposure; resistance; transgenic plant; ACC;  
 KW 1-aminocyclopropane-1-carboxylic acid biosynthesis; ds.  
 XX  
 OS Poplar nigra.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 119..1579  
 FT /\*tag= a  
 FT /product= PNACCS2  
 XX  
 PN JP09075088-A.  
 XX  
 XX 25-MAR-1997.  
 PD  
 XX  
 XX 07-SEP-1995; 95JP-0254510.  
 PF  
 XX  
 PR 07-SEP-1995; 95JP-0254510.  
 XX  
 XX (TOYT ) TOYOTA JIDOSHA KK.  
 PA  
 XX WPI; 1997-239270/22.  
 DR P-PSDB; AAW21755.  
 DR  
 XX  
 PT Ozone-Induced 1-amino:cyclopropane-1-carboxylic acid synthetic  
 PT enzyme genes - from poplar tree, are useful for generating  
 PT ozone-resistant trees and pollution clean-up trees  
 XX

PS Claim 2; Pages 9-11; 12pp; Japanese.

CC This sequence, designated PNACCS2, is a 1-aminocyclopropane-1-  
 CC carboxylic acid (ACC) synthase gene isolated from poplar trees which  
 CC had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone  
 CC for 6 hours after one hour acclimation at 25 degrees C, 70 % relative  
 CC humidity, 30 k lux and air current 30 cm/second. This gene will be  
 CC useful for breeding air pollutant ozone-resistant trees, especially  
 CC poplar.

SQ Sequence 1868 BP; 590 A; 366 C; 405 G; 507 T; 0 other;

Query Match 36.0%; Score 691.6; DB 18; Length 1868;  
 Best Local Similarity 71.7%; Pred. No. 2.8e-189;  
 Matches 923; Conservative 0; Mismatches 359; Indels 6; Gaps 1;

QY 119 tgttgcacaagatggcttgggtgagcatgacatgcgaatcatcccatcttctggtat 178  
 Db 138 ttttgcacaagattgcaagaatgtagacatggagagaactccccatattttgtagat 197  
 QY 179 ggaaggcttatgatcaaaacccctttcatccacagataatcctaacggttgttatgcaa 238  
 Db 198 ggaagcttacgataaaaaacccctttccactactgacaaccccgatggagtaatacaa 257  
 QY 239 tgggtctgtgagaatcagcttacctctgatttgggtgaagattgtagatactgaacaac 298  
 Db 258 tgggtctagcagaaaatcagcttccgctgattcgattagactggaatcaagaacatc 317  
 QY 299 ctgaagctccatttgcactccagaagaataaatatttcaggccatgacgttaacttc 358  
 Db 318 ccaaaagctccattgcaatccctgaaggagttcattgttcaaggattgtgtaacttc 377  
 QY 359 aggtattatcatgtctgcccaggttcagaaatgctgtggctaaatttatggctagaacaa 418  
 Db 378 aggtattatcatggtctgccagagtttcgacaggctattggaagtttatggggagatta 437  
 QY 419 ggggaaacagaatcacgttttgacccctgacgtatttgcagagcgggtggagccaccggag 478  
 Db 438 gaggagaaaggtgacatttgaccagatcgcatagtcagtcagcgggtggagcaactggag 497  
 QY 479 cacagaagtcaactgcttgggttggcagatcccgccgagcattctttagtgcctatc 538  
 Db 498 caaacgagctgacatgtttgctgcccagatcccggggagcttcttctgttctctc 557  
 QY 539 cctattatccaggcttbgaccgggattgaggtggaacaggaggttaactttgttcag 598  
 Db 558 ctactatcctgattctatcgagaccttgatgctgacgtgggttcagattgttcag 617  
 QY 599 ttatgtgcgtagctcaaaataattctgttgacaaaaggagcatttgaagatgctcatg 658  
 Db 618 ttgactgcgtagatcacaactttccagatcacaagaatgtagcgtggaagcagcatatg 677  
 QY 659 agaaagcaagagaggaataacatcagatgataaagggtttacttgatcaccaatccatcaatc 718  
 Db 678 ataaggcacaacaggatggcatcaatgtcaaggcttaataatacaaaacccatcaatc 737  
 QY 719 cattaggcacaatcatcagacagaaaagacactgagaaacgggtggtgagcttcatcaatgaga 778  
 Db 738 cacttggcaccacttggacagagacactaaagtgcctctgtgagcttcatcaatgaga 797  
 QY 779 agcgtatccacctgtatgtagaaatatatgctgcaacagtttttcagcacaacccgggtt 838  
 Db 798 aaacatacacatagctctgcgtgaaatttatgctgcgaccatcttcagctcccgaaatt 857  
 QY 839 tcataagcatagctgagatatttagaggatgaacacagacatagagtgtagccgcaactcg 898  
 Db 858 tcgtaaagcgtttctgaggttatagaaga-----ggtcaggttgcaacogtgacatca 911  
 QY 899 tacacattgtttatagcttcttcaaaagacatgggggttccctggcttcagagtagcggaatca 958  
 Db 912 ttcacattgtttacagctctgccaaggacatggggaactccctggcttcagagttggaattg 971





Db 309 tctttaaacaccacaagcctccatttgcacagcacaaaggtctgcaagaattcaagaca 368  
Qy 347 tagctaaatttcagagattatcatgtctctgcccagagttcagaatctgtg-tggctaaattt 405  
Db 369 ctgcaatcttcaagattaccattggt-cttgcagagttcagatgtctgttgcaaatctc 427  
Qy 406 atggctagacaaggggaaacagaatcacgtttgacccctgacgtattgtcatgacggt 465  
Db 428 atgggaaaggtgagagggaaacagagtaacttaacccagatcgcatgattagcgga 487  
Qy 466 ggagccacgggagcacacgaagctcactgctcttgtttggcagatcccgccgagggcattc 525  
Db 488 ggagcaactggagctcatgaaatgattctctgtttgttgctgctctgctggcagatcttt 547  
Qy 526 ttatgtgccattccctattatccaggctttaccggggtttgaggtggagagacaggatt 585  
Db 548 ctgtgcccaactccctattatctctgattgattgagagcctgaggtggagaaactggtg 607  
Qy 586 aaacttgttccc--agttatgtcgatagctcaaatatttctgtgttgacaaaggaagca 642  
Db 608 cagctaaattccctgtagtagctgtgaaagtgaacaaatttcaggatcccccgaagtgc 667  
Qy 643 ttggagatgctctatgagaaagcaagagagagataacatcacagagtaaggggtttactgac 702  
Db 668 ttagaagaagcctatgagagagctcaagagagacagattagatgaaggattgctcata 727  
Qy 703 acaatccatcaaatccattagggacaaatcatctggacagaaagacactgagaaacctgggtg 762  
Db 728 acaaacccatcaaacccactaggaactatcctctggacagagagacactagctcagctagt 787  
Qy 763 agcttcatcaatgagaagcgtatccacttgcacttctgtgtgataatattctgtcacaagtt 822  
Db 788 agcttcatcaatgaaaagaaacttgcacttctgtgtgtgataatattctgtcacaagtt 847  
Qy 823 ttacagccacccggtttcacaagcactgagtagctgagattagagattgaaacagacatagag 882  
Db 848 ttctctcagccgcttctgttagcattgtctgaggtattatgagcaagaga---acgtttcg 904  
Qy 883 tctgacccgaacctctgacacattgtttatgtctcttcaaaagacatggggttccctggc 942  
Db 905 tgcacacggcactcatccacttctctacagcctgtccaaggacatgggttccctggc 964  
Qy 943 ttacagagtcgcatcatatctcttcaaatgattgtgtgttaattgtgcacgcaaaatg 1002  
Db 965 ttacaggggtgggattgtctcacttccatcaatgacgaggtgtgtaattgtgcggaagatg 1024  
Qy 1003 tcaagctttggattggtgtcaacacagactcagtagtcttttagctcagctgacttaaatgat 1062  
Db 1025 tcaagtttcggctgtatccacacaaactcagcactaatcgcatcaatgctctcggac 1084  
Qy 1063 gatgagtttggagaggtttctgacagagagtgcaaaagaggttggtctcaaaaggttcagg 1122  
Db 1085 gatgaattctgtgacacattcatctgtggagagcgcgaagaggtgtagcgagaggtacaca 1144  
Qy 1123 gttttcaactgggggttgccaaagtgtgcataaagtgcttcaaaagcaaatgctgtctata 1182  
Db 1145 acctcacaagagggtgtgcacaaatggaacattgtagtgcctaaagacatgggggggtta 1204  
Qy 1183 ttgtgtgagattgatttaaggaacactctcacaagcccaactctgactctgaaacggag 1242  
Db 1205 ttcatatgagtagttagagggtctctcagaaggagaagacttccgagggagagatgggt 1264  
Qy 1243 ctttggaaagtattcatcatgaagttaagatcaatgtttccacctgggttattccttccat 1302  
Db 1265 ctgtggagagtgataatcaatgaagtgaagctaaatgtgtccaggggcgctgttccat 1324  
Qy 1303 tgcactgagccaggggtgtgttgaggtgtgtctatgccaaatgatgatgctgtgcga 1362  
Db 1325 tgcctggagccaggggtgtgtgaggtgtgtcttggcaacatgatgatgacttgacgatgcag 1384  
Qy 1363 attgtttgcaacgaatccgaacttctgtcttcaaaacaaagaggtcgtgtgt----- 1417

Db 1385 gtggctctgagagagatcataaatttgcacttcagacaagaagtcggttttgcct 1444  
Qy 1418 -ctaataagaacaacatgttggcacagtaactt---gagctgagctcctcaaaacacagaag 1473  
Db 1445 gcaatcaagagacagtggttggcaaacacacttgggaagctcagcttgtcttcagagaga 1504  
Qy 1474 ttgtgatgatcacacatgtcacctcactctcccc 1507  
Db 1505 ttgtgatgttccagatgctcctcaatgtccccctc 1538

RESULT 6  
AAV20947  
ID AAV20947 standard; cDNA to mRNA; 2088 BP.  
XX  
AC AAV20947;  
XX  
DT 07-JUL-1998 (first entry)  
XX  
DE Coffee-fruit specific ACC synthase cDNA.  
XX  
KW Coffee-fruit; 1-aminocyclopropane-1-carboxylic acid synthase;  
KW ACC synthase; ethylene biosynthesis; fruit ripening; ss.  
XX  
OS Coffea arabica.  
XX  
FH Key  
FT CDS 187..1701  
FT /\*tag= a  
FT /product= ACC\_synthase  
XX  
PN WO9806852-A1.  
XX  
PD 19-FEB-1998.  
XX  
PF 11-AUG-1997; 97WO-US14184.  
PR 12-AUG-1996; 96US-0695412.  
XX  
PA (UYHA-) UNIV HAWAII.  
XX  
PI Moisyadi I, Neupane KR, Stiles JT;  
XX  
DR WPI; 1998-159543/14.  
DR P-PSDB; AAW52818.  
XX  
PT ACC synthase and ACC oxidase from coffee, Coffea arabica - and  
PT encoding DNA, useful in methods to control coffee bean ripening e.g.  
PT to allow synchronous ripening and thus more productive harvesting  
XX  
PS Claim 2; Fig 2; 72pp; English.  
XX  
CC The present sequence encodes Coffea arabica, coffee-fruit specific  
CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase.  
CC ACC synthase cDNA can be used to control ethylene biosynthesis in  
CC coffee plants, as ACC synthase is an element of the ethylene  
CC biosynthesis pathway. Transformation of wild-type coffee plants  
CC with constructs containing the cDNA in an antisense orientation  
CC can block ACC synthase synthesis. The cDNA can also be used to  
CC block ACC synthase synthesis by co-suppression. Plants transformed  
CC with the cDNA are incapable of synthesising ethylene, which is  
CC necessary in the final stages of fruit ripening in coffee,  
CC therefore ethylene application enables fruit ripening to be  
CC controlled, e.g. application to the entire plant can synchronise  
CC ripening. Coffee beans are preferably obtained from mature fruit,  
CC but non-uniform ripening has necessitated laborious hand-picking,  
CC or low yields and productivity when harvesting by strip harvesting  
CC or mechanical techniques. The ability to synchronise ripening  
CC makes mechanical harvesting more productive.  
XX  
SQ Sequence 2088 BP; 599 A; 421 C; 432 G; 636 T; 0 other;

Query Match		35.0%	Score 672.8	DB 19	Length 2088
Best Local Similarity		70.7%	Pred. No. 8,1e-184		
Matches 912		Conservative	0	Mismatches 37	Indels 6
Qy	106	gaccaaacctccctgtgtgtccaaagatggctattgggattgggacatgggcacatggcgaatacatcccca	165		
Db	208	gaaacaaacaactctgtgcgaagatggcaaccaacgatggacatgggcgaatactgcct	267		
Qy	166	tactttgatgagtggaagggcttatgatcaaaacccctttcatccacacagataaactcctaac	225		
Db	268	tattttgatggttggaaagcatatgatagtgatccttaccatccacacagaatactcctaat	327		
Qy	226	gggtttatgaaatgggtctgtgagaatcagcttaacctgtatttggttgaagattgg	285		
Db	328	gggtttatacagatgggaactcgcagaaaaatcagttatgctttgtattgctcgaggaatgg	387		
Qy	286	atactgaacaacctgaacccctccatttgcactccacagaaggaaataatgatatttcagggcc	345		
Db	388	gttcgaacaatccagggcttccatttgcacagcagaaggagcgacaataattcatggaa	447		
Qy	346	atagctaaactttcaggatattcatgtgtctggccagatccagaatgctgtggctaattt	405		
Db	448	gttgctatctatacagatattcatgtgttcgaagttccagagttccagaatgctgtagcaagttc	507		
Qy	406	atggctagaacaaggggaaaacgaatacgtttgacctgacctgtatgtcatgagcgct	465		
Db	508	atggagaaggtgagaggtgacagagtcgaattcgatcccaacccgattgtgatggagtg	567		
Qy	466	ggagccaccggagcacacgaagctactgctcttttggttggcagatcccggcagggcattc	525		
Db	568	ggggcaacccggagctcagaaactctggctctgttttagctgacctgaagatgcgttt	627		
Qy	526	ttagtgccattccctattatccaggctttgacccgggatttgaggctggagaacacagagtt	585		
Db	628	tgtgtaccacaccattatccaggatttgatcgggatttgaggctggagaacagggatg	687		
Qy	586	aaactgttccagttatgtgcgtagctcaataattctcgtttgacaagggaagcattgtg	645		
Db	688	caactcttccaaattgtttgtcgcagctccaaigatttttaaggctcaataagaatccatg	747		
Qy	646	gaagatgcctatgagaagaagagagagataaacatcagatgaataagggtttactatgacc	705		
Db	748	gaagctgtttatcagaagctcaagaagccaaatcagatgaataagggtttcctcttaaat	807		
Qy	706	aatcatcaaatccattaggaacaaatcattggacagaagaacactagaaacgctggtgagc	765		
Db	808	aatcatcaaatccattgggaactgttcttgacagggaacatttgatgatatgaca	867		
Qy	766	ttcataatgagaagcgtatccacctgtatgtgtgataaataatgtcgcacagattttc	825		
Db	868	ttcataatgacaaaaatacccacttgattgttgatgagatatttctgccacgctcttc	927		
Qy	826	agccaaacccggttcataacgatagctgagatattagaggatgaacacagatagatgt	885		
Db	928	agccagccgaattcatcagcatctctcgaaaataattggagcat-----gatgttcaatgc	981		
Qy	886	gaccgcaacctcgtacaacttgtttatagcttcttcaaaaggacatggggttccctggcttc	945		
Db	982	aacctgtatctatcatctgtgtatagctcgttccaaggacttgggcttccctggattc	1041		
Qy	946	agagtgcggcatcataactcttacaatgatgctgtgtgttaattgtgcacgcgaataatgca	1005		
Db	1042	agaattggcaatttgattcataataatcagcgtctgttcagctgtgtagaaaaaagtgcg	1101		
Qy	1006	agctttggatttgggttcaacacagactcagtatctttttagcatcgatgcttaaatgatgat	1065		
Db	1102	agtttgggctgttttcaacacaaactcagcatctctgattcgatccttggtatcggcgcaa	1161		
Qy	1066	gaatttggagaggtttcttggcagagagtgcaaaagggttggctcaaaaggtttcagggtt	1125		
Db	1162	gcatttatggacaataatcttccacgagctcagagagattagctgcaaggcatggctctt	1221		
Qy	1126	ttcaactgggggttggccaaagtgtgcataaagtctgtcgaaggaatcgtgtggtctattt	1185		

CC wounding has occurred and diminishes their post harvest quality and  
CC storage life. Novel ACC synthase genes expressed in transgenic plants  
CC using either sense or antisense expression system may be used to control  
CC the regulation of plant development, in particular fruit ripening,  
CC reducing senescence and thus improving storage life.  
XX  
SQ Sequence 1113 BP; 320 A; 212 C; 264 G; 317 T; 0 other;

Query Match 33.0%; Score 635.2; DB 18; Length 1113;  
Best Local Similarity 74.3%; Pred. NO. 4.4e-173;  
Matches 831; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

QY 235 caaatgggtcttgctgagaatacagctctaccctctgtgattggttgaagattgatactgaac 294  
DB 1 cagatgggatttggggaaatactgcttgccttgcttgattagttcaagaatgggtcttaagc 60

QY 295 aacctgaagctccattgactccagaagaataaaatgatttcaggggccatagctaac 354  
DB 61 aaccagaagctctatctgactccgaaggtataagtgatttcagagatacgtatc 120

QY 355 ttccaggattatcatgtgtgccgagttcagaaatgctgtggtctaaattttatggtcaga 414  
DB 121 ttccaggattatcacggtctgcagagttcagaaatgctgtgcaaatttttatggcaaga 180

QY 415 acaaggggaacacagatacacgtttaccctgacgtattgttgcattgagcgggtgagccacc 474  
DB 181 gtgaggggaatagatgataacacacctgatacgaattgttatgagcgtggagcaacc 240

QY 475 ggagcacacgaagtacgtcttctgttggcagatcccgcgagggcattcttagtgccc 534  
DB 241 ggagcacatgagacggttgctcttgttggctgatacccggtgaagcatttttgggtgcc 300

QY 535 attccctattatccaggttttgaccgggattgagttggtggagaaacagggagttaaactgtt 594  
DB 301 actcttactatccaggatttggtcgagatttgagattgagatggagaaacagggagttcaactttt 360

QY 595 ccagttatgtcgatagctcaaatatttcgttggatgagaaagaaagcattggaagatgcc 654  
DB 361 ccagttgtgtgagcgttctcaaatatttcgaatttcgaagaaagcgtggagcagca 420

QY 655 tatgagaagcaagagagataacatcagagtaaagggtttactgatcaccaatccatca 714  
DB 421 tatgaaaagctcaagagacacatcagaaatcaagggttggctcctcacaatacctatcg 480

QY 715 aatccattaggcaaatcatgagacagaaagacactgagaaacccgtggtgagcttcatcaat 774  
DB 481 aaccgcgtgggactgtttggacagagaacactaagaagttagtaagcttcaattaat 540

QY 775 gagaagcgtatccactgtgtatgataaataatattgctgcaacagtittca---gccaa 831  
DB 541 gaaaagaacatccactgtgtcgcagcagataattatgctgcccacatctctcatgggccag 600

QY 832 ccggttttcataagcatagctagatattagaggtgaaacacagacatagagtgcacgc 891  
DB 601 ccgatttcattagcatctctgaaattatagaaga-----agatatcactgcgaatcgc 654

QY 892 aacctgtacacattgtttatagttcttccaaaggacatggggttccctcggcttcagagtc 951  
DB 655 aatctcatccactggtttacagttcttccaaaggatctggggttcccaggcttttagggtc 714

QY 952 ggcatactactcttacaatgactgtgtggttaattgtgcacgcaaaatgtcaagcttt 1011  
DB 715 ggcatactactctacaacgatacagttgtgagttgctgcgcctgcgaatgtcaagcttt 774

QY 1012 ggatgggtgtcacacagatcagtatcttttagcatgcatgattgataatgattgatt 1071  
DB 775 ggactgtatcatcaacaactcaacatttaacgtctcaattgttatcagatgataattt 834

QY 1072 gtggagaggtttctgagagagtgcaagaggttggttcgaaggtttcagggttttcaact 1131  
DB 835 gtggataggtttacttgagagtgctaaaggcttgcaaaaggcttcgaagagccttcaca 894

QY 1132 ggggggttggccaaagtgtggcataaaagtgtcttgcaaaagcaatgctggtctatttgtgtg 1191  
DB 895 tgggggtctatctcaagttagcattgtgtgtttgaagagcaatgcggggtattttctg 954

QY 1192 atgggtattaaaggcaacttctcaaaagccaaactttcgaactctgaaacggagctttggaaa 1251  
DB 955 atggatttgcatactctcctcaaggagcaaaactgatgaagcagagataagaactgtggaaa 1014

QY 1252 gttatcatctgaagttaagatcaatgtttccactggcttcttccattccattgcaactg 1311  
DB 1015 gfgataatcaacgaagttaataatgtttctccgggttcttcttcttccattgcgcta 1074

QY 1312 ccaggtggtttgaggtgtgctatgccaaacatggatga 1349  
DB 1075 ccaggtggtttcgggttcttcgcaaatggagca 1112

RESULT 8  
AAQ15134  
ID AAQ15134 standard; DNA; 1775 BP.  
XX  
AC AAQ15134;  
XX  
DT 17-DEC-2001 (updated)  
DT 09-MAR-1992 (first entry)  
XX  
DE Clone pACC1 encoding the tomato ACC synthase.  
XX  
KW 1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening; ss.  
XX  
OS Lycopersicon esculentum c.v. Rutgers.  
XX  
FH Key Location/Qualifiers  
FT CDS 91..1548  
FT /\*tag= a  
FT polyA\_signal 1732..1737  
FT /\*tag= b  
XX  
XX USN7579896-N.  
XX  
PD 12-NOV-1991.  
XX  
PF 10-SEP-1990; 90US-0579896.  
XX  
PR 10-SEP-1990; 90US-0579896.  
XX  
PA (USDA ) US SEC OF AGRICULTURE.  
XX  
PI Theologis A, Sato T;  
XX  
DR WPI; 1991-368895/50.  
DR P-PSDB; AARI5506.  
XX  
DNA encoding ACC synthase - used for control of plant development  
and for prodn. of ACC synthase, ethylene and ethanol  
XX  
PS Disclosure; Fig 8; 73pp; English.  
XX  
XX A lambda gt10 library was constructed using cDNA prepared from polyA  
RNA isolated from powdered, frozen fruit (i.e. tomatoes).  
CC Recombinant phage containing inserts were plated, transferred to  
CC a nitrocellulose filter and hybridised to zucchini pACC1 cDNA as  
CC probe (see AAQ15131). A full-length cDNA from tomato, designated  
CC pACC1 was recovered. Additional clones were isolated using the  
CC 3'-end of pACC1 as a probe.  
CC See also AAQ15132-Q15140.  
CC (Note: Revised entry submitted to correct the patent number format of  
CC US Government-owned NTIS applications to prevent clashes with ongoing US  
CC granted patent numbers. For further information please visit the Derwent  
CC web site at [www.derwent.com/dwpi/updates/ntis\\_us.html](http://www.derwent.com/dwpi/updates/ntis_us.html).)  
XX  
SQ Sequence 1775 BP; 589 A; 279 C; 362 G; 545 T; 0 other;

[illegible]

QY	1071	tgtgagagagttcttcgacagagtgcaaaagaggttggctcaaaaggttcagggttttcac	1130
Db	1071	cgtcgataattttcttaagaagaaacgcgataaggtttaggtataaaaggcacaaacattttac	1130
QY	1131	tgggggggttggccaaagtgtgcataaagtgcttgcacaaagcaatgcgtgtatatttgtgtg	1190
Db	1131	taatggacttgaagtgtgggaattaaatcgttgaaaaaataatgcgggggctttttgttg	1190
QY	1191	gatgatattaaagcgaacttctcaaaaagccaaacttttcgactctgaaacggagagctttggaa	1250
Db	1191	gatgatttgcgtccacttttaagggaatcgactttcgatagcgaatgtcgtataggag	1250
QY	1251	agttatcaatcagaagttaagaatcaatgtttcaccctggctattccttccattgcactga	1310
Db	1251	agttattataaacgattttaagcttaacgtctcgcctggatctctgttgaaatgtcaaga	1310
QY	1311	gcacgggtggtttaggggtgctatgccaaatcggatgatatggctgtgcacaaattgcttt	1370
Db	1311	gcacgggtggttcaggattgttttgcataatcggatgatggaacggttgatatgtcgct	1370
QY	1371	gcacgaatccgcaactttgt-----gcttcaaaaacaaaggagtcgtggtgtc	1418
Db	1371	cgcgaggattcggaggttcgttaggttgagaaaagtgagataaaatcgagttcgtatgga	1430
QY	1419	taataagaacaatttggcacagataacttgagctgagcctcaaaacacagaaggtttga	1478
Db	1431	aaagaagaacaatggagaagaataatttgagacttagttttcgaagaagaatgatga	1490
QY	1479	tgatatcaccatgtcacctcacctctcccc	1507
Db	1491	tgaagtggtttgtcaccactttcgtcac	1519
RESULT 9			
AAD04546			
ID	AAD04546 standard; cDNA; 1818 BP.		
XX	AAD04546;		
XX	04-JUL-2001 (first entry)		
DE	Tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2 cDNA.		
KW	Tomato; 1-aminocyclopropane-1-carboxylic acid synthase; LE-ACC2;		
KW	ethylene production; fruit ripening; transgenic plant; ss.		
OS	Lycopersicon esculentum.		
FH	Key	Location/Qualifiers	
FT	CDS	91..1548	
FT	/*tag= a		
FT	/product= "Tomato LE-ACC2"		
FT	/transl_except= (pos:460..462, aa:Ala)		
XX	US6207881-B1.		
XX	27-MAR-2001.		
XX	25-JAN-1995; 95US-0378313.		
PR	19-APR-1992; 92US-0862493.		
PR	10-SEP-1990; 90US-0579896.		
XX	(USDA ) US SEC OF AGRIC.		
XX	Theologis A, Sato T;		
PI	WPI: 2001-289591/30.		
DR	P-PSDB; AAE00984.		
XX	Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic		
PT	acid synthase, LE-ACC2 useful for producing ACC synthase which is		
PT	essential for the production of ethylene in higher plants.		

XX PS XX CC CC CC CC CC CC CC CC XX SQ

Claim 1; Fig 5; 92pp; English.

The present sequence is a cDNA encoding tomato (Lycopersicon esculentum) 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2. ACC synthase is capable of catalysing the conversion of AdoMet (S'-adenosyl methionine) to ACC and methyl thioadenosine (MTA). ACC DNA is useful for producing ACC synthase which is essential for the production of ethylene in higher plants, where ethylene is a determinant of fruit ripening. The ACC DNA is also useful for producing transgenic plants which are overproducers of or are deficient in ACC synthase.

Sequence 1818 BP; 602 A; 282 C; 367 G; 567 T; 0 other;

Query Match 32.8%: Score 630.2: DB 22: Length 1818:

Best Local Similarity 65.48; Pred. No. 1.6e-171;

Matches	961;	Conservative	0;	Mismatches	493;	Indels	15;	Gaps	2;
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Qy	51	acttttttacctccacactcttaaccacatacacaccataatggttttccaaggccatggacca	110
Db	54	aattttcacttctaactcatttagtaaaaaaaatgggatttgatgtgcaagac	113
Qy	111	aactcccttgttccaagaatgctattggggatggacatggcgaatccatccccatactt	170
Db	114	caactcaatcttatcaaaaatgggtactaatgaagagcatggcgaaaaactcgccatactt	173
Qy	171	tgtatggatgaagccttatgatcaaaaccccttctatccacacagataactcctaaccgtgt	230
Db	174	tgtatggatgaagcagacagatagatcctttccacctctaaaaaaacccaacgagat	233
Qy	231	tatgcaaatgggtttgtgtgagaatcagcttaacctctgatatttggttgaagattggatact	290
Db	234	tatcccaatgggtctgtgataaatcagcttgtttgacctgtatagatagagattggattaa	293
Qy	291	gaacaaacctgaagctccatttgcactccagaagaataaaatgatattcagggccatagc	350
Db	294	gagaaacccaaggttcaattg----ttctgaaggaatacaaatcatctcaaggccattgc	350
Qy	351	taactttcaggattatcatggtctggccgagtttcagaaatgctgtggtcctcaaatattatgc	410
Db	351	caactttcaagattatcatgctgctgaattcagaaaaagcattgcgaaatttatgga	410
Qy	411	tagaacaaggggaaaacagaatacagctttgacctgacctgattgttcattgagcgggtgagc	470
Db	411	gaaaacagggaggaagagttagattgtatccagaagagttgttatggttgggtgtgc	470
Qy	471	cacggagacacagaagctactgccttttgtttggcagatcccgcgagagcattcttagt	530
Db	471	cacttggagctcaatgagacaattatatttgtttgggtgactctcgcgatgcatcttttag	530
Qy	531	gccattccctattatccaggcttgcacgggatttggaggttggaggaacagaggttaact	590
Db	531	accttcaactactaccacagatatttaacagagattttaagatggagaaacttggagacact	590
Qy	591	tgttccagtttatgtgcgatagctcaataaattctgtgtgacaaaaggaagcatttggaga	650
Db	591	tattccaattcactgtgagagctccaataatttcaaaattacttcaaaagcagtaaaaga	650
Qy	651	tgcctatgaaagaagcagaagagataaacatcacagataaagggttttactgatcaaccaatcc	710
Db	651	agcatatgaaatgcaaaaaatcaaacatcaaaatgaaagggtttgtatttggaccaatcc	710
Qy	711	atcaaatccattaggcacaatcatgacagaaagacactgagaaacggttggtagcttcat	770
Db	711	atcaaatccattgggcccactttgacaaagacacactgaaagtgcttctgagttctcac	770
Qy	771	caatgagaagcgtatcaccttgtatgtatgaaatatatgctgcacacagttttcagcca	830
Db	771	caaccaacacaacatccacttgtgtgacgaaatctacgcagccaactgttcttgaac	830
Qy	831	acocgggtttcataagcatagctgagatatttagaggatgaaacagacatagatgtgaccg	890

XX	02-APR-1992;	92US-0862493.	
PR	10-SEP-1990;	90US-0579896.	
PR	25-JAN-1995;	95US-0378313.	
PR	07-JUN-1995;	95US-0481171.	
XX			
PA	(USDA )	US SEC OF AGRIC.	
XX			
PI	Sato T,	Theologis A;	
XX			
DR	WPI;	1998-206005/18.	
DR	P-PSDB;	AAW47313.	
XX			
PT	DNA encoding anti-sense RNA blocking plant ACC synthase expression -		
XX	is used for producing transgenic plants with delayed fruit ripening		
PS	Example 3;	Columns 63-68; 91pp; English.	
XX			
CC	The present sequence encodes tomato		
CC	1-aminocyclopropane-1-carboxylic acid (ACC) synthase. Tomato ACC		
CC	synthase was used in the isolation of conserved sequences from		
CC	five tomato (LE-ACC 1A, LE-ACC 1B, LE-ACC2, LE-ACC3 and LE-ACC4)		
CC	and two zucchini (CP-ACC 1A and CP-ACC 1B) ACC synthases.		
CC	A novel DNA molecule comprises an expression system which, when		
CC	contained in a plant host cell, generates RNA that is sufficiently		
CC	complementary to an RNA transcript of an endogenous ACC synthase		
CC	gene to prevent its synthesis. The expression system consists of		
CC	the reverse transcript of the antisense RNA (i.e. cDNA) operably		
CC	linked to control sequences that effect its transcription into the		
CC	antisense RNA, where the cDNA can be amplified from the endogenous		
CC	ACC synthase gene by primer pairs encoding conserved ACC synthase		
CC	sequences. The DNA molecule can be used to delay ripening of		
CC	tomato or zucchini fruits.		
XX			
SQ	Sequence 2230 BP; 824 A; 314 C; 414 G; 678 T; 0 other;		
Query Match			
Best Local Similarity 32.8%; Score 630.2; DB 19; Length 2230;			
Matches 961; Conservative 0; Mismatches 493; Indels 15; Gaps			
QY	51	acttttttacactccacactcacaaccatacacccatattgggtttcgaagccatggacca	110
DB	54	aatttcttcactcttaaacactatttagtaaaaaaaatgggatttgagattgcaaaagac	111
QY	111	aactcccttggtgtccagatggcgtattggggatggacatggcgaatcatccccatactt	170
DB	114	caactcaactctatcaaaaattgggtactaatgaagcatggcgaaaactcgccatatatt	173
QY	171	tgatggatgggaaggtctatgatcaaaaccccttcatccacagataactcctaaccggtgt	230
DB	174	tgatgggtgggaagcatcagatgatcctttccaccctctctaaaaaccccaagcgagt	233
QY	231	tatcgaatgggtcttctgagaaatcagcttacctctgatttggttgaagattgatact	290
DB	234	tatccaaatgggtctgtgtaaatcagcttgtttagacttgatagaagattgatttaa	293
QY	291	gaacaacccctgaagccctccatttgcactccagaaagaaataatgattccagggccatagc	350
DB	294	gagaaaccccaaaaggttcaatttg---tctgaaggaaatcaaatcattcaagggccattgc	350
QY	351	taactttcaggaatatatggtgtctggccgagttcagaaatgctgtggctaaatttatggc	410
DB	351	caactttcagatttatcatggtctgctgaattccagaaagcagattgcgaaattcatgga	410
QY	411	tagaacaaggggaaacagaatacagtttgacctgacogtatttgtcatgagcggtgagac	470
DB	411	gaaaaacaaggggaagagagttagattttgatccagaaagagttgttaTggttggtgtgc	470
QY	471	cacggtgacacacgaagtcactgaccttttggttggcaatccccggcaggcattcttagt	530
DB	471	cactggagctaatgagacaattatatttggttggctgatcctggcgatgcatttttagt	530

RESULT 11  
AAD04544  
ID AAD04544 standard; DNA; 2230 BP.  
XX

QY	531	gccattccctattatccaggctctgacggaatttgaggtggagaaacaggagttaaact	590
Db			
Db	531	acctcaccatactaccagcattaacgagatttaagatggagaaactggagttacaact	590
QY	591	tgtccagttatgtgcgatagctcctaaataatttcgtgtgacaaggaagcattggaaga	650
Db			
Db	591	tattcctaattcactgtagagctcccaataatttcaaaatactccaagcagtaaaaga	650
QY	651	tgccattgagaagcaagagagagaataacatacagatcaaaaggttttactgatcccaatcc	710
Db			
Db	651	agcatatgaaattgcacaaaatacaactcaagataaaagtgttgatttgaccaatcc	710
QY	711	atcaatccattaggccaatacatgatgacagaagacactgaaacccgttgtagattcaat	770
Db			
Db	711	atcaatccattggccaccactttggacaagacacactgaaaagtgtccttgagtttcaac	770
QY	771	caatgagaagcgtatccacccttgtagtgaaatatctgctgcacacagttttcagcca	830
Db			
Db	771	caaccaacacacaatccaccctgtttgtgagaaatctacgcaccactgctttgacac	830
QY	831	accgggtttcataagcatagctgagatattagagatgaaacacacatagagtgtagccg	890
Db			
Db	831	gcctcaattcgtcagtagtagtgaaatccctcgatgaacaggaaatgacttactgacaaa	890
QY	891	caactcgtacacattgttttagtctttcaaaagacatgggttccctggcttcacagtt	950
Db			
Db	891	agatttagttcacatcgtctacagctcttcaaaagacatgggtttacagagatttaggt	950
QY	951	cggcatcatatcactttacaatgatgctgtgtggttaattgtgcacgcaaaatgtcgaagctt	1010
Db			
Db	951	cggaaatcatatattcttttaacgcagatgcgttaattgtctagaaaaaatgtcgagttt	1010
QY	1011	tggaattggtgtcaacacagactcagttatcttttagcatcgatcgtactaaatgatgatagtt	1070
Db			
Db	1011	cggtttagttatctacacaaacgcaatatcttttagcggcaatgctatcgacgaaaaaatt	1070
QY	1071	tgtagagaggtttctcggcagagagtgcaaaagaggttggctcaaaaggttcagggtttttcac	1130
Db			
Db	1071	cgcgataattcttaagaaagacgcgatagaggttaggttaaaaggcacaacattttac	1130
QY	1131	tggggggttggcacaagtttgccataaagtcgtctgcacaaacatgctggtctatttgtgtg	1190
Db			
Db	1131	taatggacttgaagtagtgggaattaaaatgcttgaaaaataatcggggctttttgtgtg	1190
QY	1191	gatggatttaaggcaacttctcnaaaagccaactcttcgactctgaaacggaggtcttgaaa	1250
Db			
Db	1191	gatggatttgcgtccacttttaagggaatcgactttcgatagcgaatgtcgttatcgag	1250
QY	1251	agttacattcatgaagttaaagatcaaatgtttcaacctggctattccttccattgcactga	1310
Db			
Db	1251	agttattataacagatgttaagcttaacgctcccgctggatcttcgtttgaatgtcaaga	1310
QY	1311	gccaggttggttaggggtgctatgccaacatgagatgatattggtgtgcacaaattgcttt	1370
Db			
Db	1311	gccaggttggttccgagttgttttgcaaatatgatgatggaaacggttgatcattgcgct	1370
QY	1371	gcaacgaatccgcaacttgt-----gcttcaaaacaggaggtcggtggtgtc	1418
Db			
Db	1371	cgcgaggtattcggaggttcgtaggtgttgaaaaagtgagataaaatcgagttcgatga	1430
QY	1419	taataagaaaacattgttggcacagtaaccttgagcttgagctcctcaaaacagaaagtttga	1478
Db			
Db	1431	aaagaagcaacaaatggaagagaataatttgagacttagtttttcgaaaagaatgtatga	1490
QY	1479	tgatatcaccatgtcaactcactccccc	1507
Db			
Db	1491	tgaagtgttttgcacacacttttcgtcac	1519

RESULT 11  
AAD04544  
ID AAD04  
XX







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QY 1251 agttatcattcatgaagttaagatcaatgtttccacctggctattcttcccttcattgcaactga 1310
DB 1251 agttattataaacagatgttaagcttaacgtctcgcctggatctctcgttggaatgtcaaga 1310

QY 1311 gccagggtgttttaggtgtctatgccaaactggatgatattgctgtgcaaatgtcttt 1370
DB 1311 gccagggtgttttaggtgtctatgccaaactggatgatattgctgtgcaaatgtcttt 1370

QY 1371 gcaacgaatccgaactttgt-----gcttcaaaaacaaaggaggtcgtgtgtc 1418
DB 1371 cgcgaggttcggaggttcgttaggtttgagaaaagtggagataaaatcgaggtcgatgga 1430

QY 1419 taataagaacattgttggcacagtaacttgagctgagcctcaaacacagaaggttga 1478
DB 1431 aaagaagcaacaatgaagaagaataatttgagacttagttttcgaagaagaatgtatga 1490

QY 1479 tgatatcaaatgtcaactcactctcccc 1507
DB 1491 tgaaggtttgtcaccactttcgcac 1519

RESULT 13
AAV09713
ID AAV09713 standard; DNA; 1800 BP.
AC AAV09713;
XX
DT 19-MAY-1998 (first entry)
DE ACC synthase DNA.
KW 1-aminocyclopropane-1-carboxylic acid deaminase; ACC deaminase;
KW fruit ripening; ethylene production; ACC synthase; ds.
XX
OS Unknown.
XX
FH Key Location/Qualifiers
FT 154..1611
CDS /*tag= a
/*product= ACC synthase
XX
XX US5702933-A.
XX
XX 30-DEC-1997.
XX
XX 06-NOV-1995; 95US-0553943.
XX
XX 17-DEC-1991; 91US-0809457.
XX 26-DEC-1990; 90US-0632440.
XX 06-NOV-1995; 95US-0553943.
XX
XX (MONS ) MONSANTO CO.
XX
XX Kishore GM, Klee HJ;
XX
XX WPI: 1998-076419/07.
XX P-PSDB; AAW39423.
XX
XX Production of plants with delayed ripening - using DNA encoding
XX 1-amino:cyclo:propane-1-carboxylic acid deaminase
XX
XX Example 7; Column 29-34; 56pp; English.
XX
XX This DNA sequence encodes an ACC synthase gene which is used in
XX a novel method for producing fruit-bearing plants with delayed ripening.
XX The method involves the expression of a 1-aminocyclopropane-1-carboxylic
XX acid (ACC) deaminase gene in a plant at a level sufficient to reduce
XX ethylene production in the fruit.
XX
XX Sequence 1800 BP; 602 A; 284 C; 360 G; 554 T; 0 other;
XX
XX Query Match 32.6%; Score 627; DB 19; Length 1800;

```

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Best Local Similarity 65.3%; Pred. No. 1.3e-170;
Matches 959; Conservative 0; Mismatches 495; Indels 15; Gaps 2;

QY 51 acctttttcacctccacacataaccacacataccacataatgggtttcaaggccatggacca 110
DB 117 aatttctctctctaaactcatttagtaaaaaaaatgggatttgagattgcaagac 176

QY 111 aactcccttctgtccaaagatggctatttggggatggacatggcgaatacatccccatactt 170
DB 177 caactcaattcttcaaaatggctactaatgaagagatggcgaataactgcgcataatt 236

QY 171 tgaaggatggaaggtcttatgatcaaaacccctttcaccacacagataatcctaagcgtgt 230
DB 237 tgaaggatggaagcacaacagatagatcctttccaccttcaaaaccccaacggagt 296

QY 231 tatgcaaatgggtctgtctgagaatcagcttacctctgatttgggtgaagatttgatact 290
DB 297 tatccaaatgggtctgtgtaaatcagctttgttagacttgatagaagattggattaa 356

QY 291 gaacaacctgaagcctccatttgcactccagaagaataaattgatttcaggggccatagc 350
DB 357 gagaaccccaaaaggttcaatttg---ttctgaaggaaatcaaatcattcaaggccattgc 413

QY 351 taactttcaggattatcatggtctgcccaggttcagaaatgctgtgctaaatttatgac 410
DB 414 caactttcaagattatcatggtctgctgaattcagaaaagcgttgcgaatttatgga 473

QY 411 tagaacaaggggaaaacagaatcacgtttgacctgacgtatttgcattgacggctggagc 470
DB 474 gaaaacaaggaggagagagtagattgatccagaagagttgttatggctgtgtgac 533

QY 471 caccggagacacagaagtcactgctcttttggcgagatccccggcaggagcattctagt 530
DB 534 cactggagcgaatgagacaattatatttgttggctgactgctgctgagcattttagt 593

QY 531 gccattccctattatccaggcttgcacgggttgcacgggttggaggagacagaggttaact 590
DB 594 acctcaacatactaccacagcatttaacagagatttaagatggagagactggagcacact 653

QY 591 tgttccagttatgtgcgatatgctcaataatttgcgtttgacaaaagaagcattggaga 650
DB 654 tattccaattcactgtgagagctccataatttcaaaattacttcaaaaagcagtaaaaga 713

QY 651 tgctatgagaagaagaagagagataacatcagatcagagtaaaagggtttactgataccaatcc 710
DB 714 agcatatgaaaatgcacaaaatacaaacatcaaaagttgtttgttttgacaaatccc 773

QY 711 atcaaatccatttaggcacaatcatggacagaagaacactgagaaacggttgagcttcat 770
DB 774 atcaaatccatttggcacaacttggacaaagacacactgaaaagtgtcttgagtttcaac 833

QY 771 caatgagaagcgttatccaccttgcattgatgaaatatatgctgcaacagttttcagcca 830
DB 834 caaccaacacacataccacctgtttgtgacgaaatctacgagccactgtctttgacac 893

QY 831 acccggtttcataagcattagctagatattagaggatgaaacacacatagatgtgaccg 890
DB 894 gcctcaattcgtcagtatagctgaaatccctcgatgaacaggaatgacttactgacaaca 953

QY 891 caactcgtacacattgtttatagcttttcaaggacatgggttccctggcttcagagt 950
DB 954 agatttagttcacatcgtctacagcttttcaaaagacatgggtttcaccagagatttaggt 1013

QY 951 cggcatcatactcttacaatgatgctgtgtgttaattgtgcacgcgcaaaatgtcaagctt 1010
DB 1014 cggaaatcataattcttttaacgacgattcgcttaattgtgctagaaaaatgtcagattt 1073

QY 1011 tggattggtgtcaacacacagactcagttatcttttagcatcgatgctaaatgatgatgtt 1070
DB 1074 cggtttagtatctacacaaacgcaaatatttttttagcggcgaatgcatcgacgaaaaatt 1133

QY 1071 tftggagaggttttctggcagagatgcaaaagggttggctcaaaaggttccagggttttccac 1130

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Db 1134 cgtcgataattttctaagagaaagcgcgatgaggttaggttaaaagggcaacaattttac 1193  
Qy 1131 tggggggttgccaaagtggcataaagtgtcttgcaaaagcaatgctgtctatttgtgtg 1190  
Db 1194 taatggacttgaagttagtgggaattaaatgcttgaaaaataatgcgggctttttgttg 1253  
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Qy 1311 gccagggttggtttaggtgtgctatgccaacatggtgatgctgtgctgcaaaattgcttt 1370  
Db 1374 gccagggttggttcgagttgttttgcgaatatggtatggaacggttgatatgtgcct 1433  
Qy 1371 gcaacgaatcgcgaactttgt-----gcttcaaaacaaaggaggtcggtgtc 1418  
Db 1434 cgcgaggattcggagggttcgtaggtgttgagaaaagtggagataaactcaggttcgatgga 1493  
Qy 1419 taataagaacaactgttgccacagtaacttgagctgagcctcaaaacagaaagtttga 1478  
Db 1494 aaagaagcaacaatggaagaagaataatttgagacttagtttttcgaaaaagaatgcatga 1553  
Qy 1479 tgatatcaccatgtcacctcactctccc 1507  
Db 1554 tgaaagtgtttgtcaccactttcgtcac 1582

RESULT 14  
AAV30325 standard; cDNA; 2678 BP.  
XX  
AC AAV30325;  
XX  
DT 28-SEP-1998 (first entry)  
XX  
DE Pelargonium l-aminocyclopropane-1-carboxylase synthase cDNA.  
KW ACC synthase; l-aminocyclopropane-1-carboxylate synthase;  
KW ethylene; transgenic plant; wilting; geranium; pPHSacc44; ss.  
XX  
OS Pelargonium x hortorum cv. Sincerity.  
XX  
FH Key Location/Qualifiers  
FT CDS 39..1487  
FT /\*tag= a  
FT polyA\_signal 1849..1854  
FT /\*tag= b  
FT polyA\_signal 2635..2640  
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FT misc\_feature complement (1..50)  
FT /\*tag= d  
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FT /\*note= "any contiguous 50 nucleotides (Claim 12)"  
XX  
PN WO9814465-A1.  
XX  
XX 09-APR-1998.  
PD  
PF 30-SEP-1997; 97WO-US17644.  
XX  
PR 01-OCT-1996; 96US-0724194.  
XX (COLS ) UNIV COLORADO STATE RES FOUND.  
XX Ranu RS;  
DR  
DR WPI; 1998-260994/23.  
XX P-PSDB; AAW60234.  
PT New isolated ACC synthase genes - are obtained from geranium and  
PT rose, used to develop products for producing plants with reduced  
PT ethylene levels, for increasing shelf-life  
XX  
PS Claim 1; Fig 4; 77pp; English.  
XX  
CC This cDNA clone, designated pPHSacc44 (ATCC 98178), codes for a  
CC 54.2 kDa l-aminocyclopropane-1-carboxylate synthase (ACC synthase)  
CC (see AAW60234) of geranium (Pelargonium x hortorum cv. Sincerity).  
CC High quality mRNA was obtained from flower tissue using a novel  
CC adaptation of the 2-butoxyethanol precipitation technique. This  
CC was converted to cDNA and screened with a probe generated by PCR  
CC amplification (see AAV30328-29). The pPHSacc44 clone was obtained.  
CC Pelargonium ACC synthase cDNA clones pHSacc41 (see AAV30324) and  
CC pHSacc49 (see AAV30326), and rose ACC synthase cDNA clone prosekacc7  
CC (see AAV30330), are also claimed. These ACC synthase genes, or their  
CC fragments, when introduced in antisense orientation under control  
CC of a strong promoter, can be used to genetically modify a plant.  
CC especially geranium, rose or woody plant. As a consequence, the  
CC amount of ACC synthase produced in the plant cells is reduced and  
CC the rate of ACC conversion to ethylene decreases. This can be used  
CC to prolong the shelf-life of cut flowers and to reduce leaf  
CC yellowing and petal abscission during shipping and storage.  
XX  
SQ Sequence 2678 BP; 738 A; 550 C; 687 G; 703 T; 0 other;  
  
Query Match 32.6%; Score 627; DB 19; Length 2678;  
Best Local Similarity 66.6%; Pred. No. 1.6e-170;  
Matches 913; Conservative 0; Mismatches 455; Indels 3; Gaps 1;  
  
Qy 122 tgtccaagatggctattggggatggagatggcgagatcatccccatactttgtatggatgga 181  
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Qy 182 aggccttatgatcaaaaccccttccacacagataaactcaacggtgtgtatgcaaatg 241  
Db 124 aggccttatgacggtgatcggttccatccggttcacgaatcctcaacggtgttcccgatgg 183  
Qy 242 gtcctgtgagaatcagcttacctctgatttgttggaagatggatcactgaacaacctcg 301  
Db 184 gtttagctgaaaaatcagctttcatctgactgtgatggaagatgggtgaggtccaacccag 243  
Qy 302 aagcctccatttgactccacgaaggaataaatgatttcaggggccatagctaaactttcagg 361

Db 244 aagcctcaatctgacactctagaaggagttgttaagtccaaggagcgtagtcaacttttcagg 303  
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Qy 482 acgaagtcaactgccttttttggcagatcccgcgagggcattcttagtgccttccct 541  
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Db 604 aagcaagaagaacataaagcgttaaaaggcgtgctcttaaccaacccatcgaaacctc 663  
Qy 722 taggcacaatcattggacagaaaacactgagacccgttggtgagcttctcatcaatgagaac 781  
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Qy 782 gataccacttgatgtatgataaataatctgctcaacagtttttcagcaaacccggtttca 841  
Db 724 acatccacttgatcagcagaaatctacgcgcacacgcttttgcgcgcccggagttcg 783  
Qy 842 taagcatagctgagatattagagatgaacacagacatagagtgagcgaacacctgcac 901  
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Db 1321 gggcgtttgtggggaagaaggaggtggtccggtgaagagaaagaggttcatgacaacc 1380  
Qy 1442 gtaacttgagcgtgagcgtcctcaaacacagaaaggtttgtgatcatcaccatgt 1492  
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RESULT 15  
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ID AAT66246 standard; DNA; 1934 BP.  
XX  
AC AAT66246;  
XX  
DT 28-JUL-1997 (first entry)  
XX  
XX ACC synthase GAC-1 DNA.  
XX  
KW ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; antisense;  
KW ethylene; transgenic plant; Pelargonium x domesticum;  
KW in vitro propagation; tissue culture; ripening; ss.  
XX  
OS Not identified.  
XX  
FH Key Location/Qualifiers  
FT CDS 80...1528  
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XX  
PN WO9717429-A1.  
XX  
PD 15-MAY-1997.  
XX  
PF 08-NOV-1996; 96WO-US17954.  
XX  
PR 09-NOV-1995; 95US-0555755.  
XX  
XX (OGLE-) OGLEVEE LTD.  
XX (PENN-) PENN STATE RES FOUND.  
XX  
XX Arteca J, Arteca RN, Oglevee-O'Donovan W, Stoots E;  
XX  
XX WPI: 1997-281019/25.  
XX  
XX P-PSDB; AAW09878.  
XX  
XX Commercial propagation of transgenic plants by tissue culture -  
XX especially Pelargonium x domesticum with decreased ethylene  
XX formation  
XX  
XX Claim 13; Page 22-23; 36pp; English.  
XX  
XX 2 DNA sequences (AAT66246-47) respectively code for  
XX 1-aminocyclopropane carboxylase synthases (ACC synthase) GAC-1  
XX (AAW09878) and GAC-2 (AAW09879), enzymes involved in the biosynthesis  
XX of ethylene in plants. In a method for the commercial production  
XX of transgenic plants, Agrobacterium vectors carrying antisense  
XX genes for ACC synthase or ACC oxidase (see also AAT66248) are used  
XX to inoculate petiole explants of a mother plant, pref.  
XX Pelargonium x domesticum. The resulting callus is cultured and  
XX used to regenerate transgenic plants. The antisense genes prevent  
XX ACC synthase or ACC oxidase expression and hence ethylene  
XX formation and fruit ripening.  
XX  
XX Sequence 1934 BP; 498 A; 422 C; 512 G; 502 T; 0 other;

Query Match 32.5%; Score 625.4; DB 18; Length 1934;  
Best Local Similarity 66.5%; Pred. No. 3.9e-170;  
Matches 912; Conservative 0; Mismatches 456; Indels 3; Gaps 1;

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QY 182 aggccttatgatcaaaacccctttccatccacagataaattcctcaacagtggttatgcaaatgg 241  
DB 165 aggccttatgacgctgatccgttccatccgtctcagaatcctcaacggtgttatccagatgg 224  
QY 242 gtctgctgagaatcagcttacctctgattgtgttggaagattggatactggaacaacctcg 301  
DB 225 gtttagctgaaaatcagcttctcatctgacttgattgaagattgggtgaggtccaaacccag 284  
QY 302 aagcctccatttgccctccagaaagaaataaattgattcaggggccatagctaaacttttcagg 361  
DB 285 aagcctccatttgccctccagaaagaaataaattgattcaggggccatagctaaacttttcagg 344  
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DB 405 gcgggaaggtcacatttgatcccgaccgtgctgcatgagcggcgaggccaccggagcca 464  
QY 482 acgaagtcactgcctttgtttgttcgagatcccgggcgaggcatttcttagtgcccattccct 541  
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DB 645 aagcacaagaagcaacataaaacgttaaaagcggtgctcttaaccacaacccatcgaaacctc 704  
QY 722 taggcacaatcatggacagaagacacactgagaacccgtggtgagcttcatcaatgagaagc 781  
DB 705 tagacacaatctcggaccgacactctcaagagcatcgctcagctctgacccgacaca 764  
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QY 1202 ggaactctcaaaagccaactttcgactctgaaacggagcctttggaaagtattatctc 1261  
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QY 1442 gtaacttgagggtgagcctcaaaaaccagaaggttttgatgatatacccatgt 1492  
DB 1422 ttaacctcaggtgagcttctcgtcgtaaagggtacagatgagagtgatgt 1472

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Job time: 9562 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 23:24:09 ; Search time 96.17 Seconds  
(without alignments)  
4911.648 Million cell updates/sec

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Sequence: 1 atctctctccacttactt.....aggcttcaaatcttcc 1923

Scoring table: IDENTITY\_NUC  
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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
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Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	735	38.2	1888	1	US-08-485-107-1
2	686.4	35.7	1878	1	US-08-724-194-3
3	673.8	35.0	2040	2	US-08-695-412B-11
4	635.2	33.0	1113	3	US-09-043-627-9
5	630.2	32.8	2230	4	US-08-378-313-24
6	627	32.6	1800	1	US-07-809-457A-8
7	627	32.6	1800	1	US-08-553-943-8
8	627	32.6	1800	5	PCT-US91-09437-8
9	627	32.6	2678	1	US-08-724-194-2
10	625.4	32.5	1945	1	US-08-724-194-1
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13	571.4	29.7	1712	4	US-09-231-240-1
14	571.2	29.7	1104	3	US-09-043-627-3
15	567.8	29.5	1096	3	US-09-043-627-7
16	537.2	27.9	1497	2	US-08-860-577-11
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19	466.8	24.3	1098	3	US-09-043-627-5
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21	408.6	21.2	7244	4	US-08-378-313-26
22	363	18.9	5613	2	US-08-463-418-1
23	305.6	15.9	968	4	US-08-846-826A-1
24	304.2	15.8	994	2	US-08-860-577-7
25	276	14.4	7587	4	US-08-378-313-22
26	274.6	14.3	9060	4	US-08-378-313-20
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30	70	3.6	159	2	US-08-463-418-3	Sequence 3, Appli
31	44.4	2.3	7218	1	US-08-232-463-14	Sequence 14, Appli
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33	39.2	2.0	800	2	US-09-086-201-7	Sequence 7, Appli
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37	35.2	1.8	5506	4	US-09-004-838-93	Sequence 93, Appli
38	34.8	1.8	2444	3	US-08-906-791-1	Sequence 1, Appli
39	34.8	1.8	2469	4	US-09-111-730-5	Sequence 5, Appli
40	34.8	1.8	2558	4	US-09-184-001-3	Sequence 3, Appli
41	34.6	1.8	4450	3	US-08-617-860B-2	Sequence 2, Appli
42	34.2	1.8	1946	4	US-09-042-225-5	Sequence 5, Appli
43	34.2	1.8	4383	6	5177307-1	Patent No. 5177307
44	34	1.8	3434	4	US-09-439-313-476	Sequence 476, App
45	34	1.8	5829	4	US-09-439-313-473	Sequence 473, App

ALIGNMENTS

RESULT 1  
US-08-485-107-1  
; Sequence 1, Application US/08485107  
; Patent No. 5767376  
; GENERAL INFORMATION:  
; APPLICANT: STILES, JOHN I.  
; APPLICANT: NEUPANE, KABI R.  
; TITLE OF INVENTION: ACC SYNTHASE GENE AND ITS USE IN PLANTS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,107  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: UH-01170  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1888 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 17..1480  
US-08-485-107-1

Query Match 38.2%; Score 735; DB 1; Length 1888;  
Best Local Similarity 70.8%; Pred. No. 1.5e-214;  
Matches 1013; Conservative 0; Mismatches 400; Indels 18; Gaps 2;  
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Db 345 GAAGAAACAGAGCTTCATTTGACCCCTGATCGGATTTGATGAGTGGAGGAGCAACTGGAG 404
Qy 479 caacgaagtcaactgcctttttgttggcagatcccgccggaggaattcttagtgcccaattc 538
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Qy 599 ttatgtgcgtagatgcataaataatttcgtgttgacaaagggaagcattgggaagatgcctatg 658
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RESULT 2
US-08-724-194-3
; Sequence 3, Application US/08724194
; Patent No. 5824875
; GENERAL INFORMATION:
; APPLICANT: RAND, RAJINDER S.
; TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
; TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SANTANGELO LAW OFFICES PC
; STREET: 315 WEST OAK STREET, STE 701
; CITY: FORT COLLINS
; STATE: CO
; COUNTRY: USA
; ZIP: 80521
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,194
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: SANTANGELO, LUKE
; REGISTRATION NUMBER: 31,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (970) 224-3100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-724-194-3
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Query Match 35.7%; Score 686.4; DB 1; Length 1878;
Best Local Similarity 70.8%; Pred. No. 1e-199;
Matches 1001; Conservative 0; Mismatches 396; Indels 17; Gaps 6;

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Db 1265 CTGTGGAGAGTGATTAATCAATGAAGCTAAATGTGTCCGCCAGGGCGTGTTCAT 1324  
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Db 1325 TGCTGGAGCCAGGCTGTTTAGAGTGTGCTTTGCCAACATGATGACTTTGACGATGCAG 1384  
Qy 1363 attgctttgcaaacgaatccgcgaactttgtgcttcaaaaacgaagaggttgggtgt----- 1417  
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Db 1505 TTTGATGATTTCAAGATGTCTCCAATGTCCCTC 1538

RESULT 3  
; US-08-695-412B-11  
; Sequence 11, Application US/08695412B  
; Patent No. 5874369  
; GENERAL INFORMATION:  
; APPLICANT: STILES, JOHN I.  
; APPLICANT: MOISYADI, STEFAN  
; APPLICANT: NEUPANE, KABI R.  
; TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT  
; TITLE OF INVENTION: DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE  
; TITLE OF INVENTION: RIPENING OF COFFEE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JONES, DAY, REAVIS & POGUE  
; STREET: NORTH POINT, 901 LAKESIDE AVENUE  
; CITY: CLEVELAND  
; STATE: OHIO  
; COUNTRY: USA  
; ZIP: 44114  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS v. 5.1  
; SOFTWARE: WordPerfect v. 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/695,412B  
; FILING DATE: 12-AUG-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US08/485,107  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRIFFITH, CALVIN P.  
; REGISTRATION NUMBER: 34,831  
; REFERENCE/DOCKET NUMBER: 265036600002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (216) 586-7050  
; TELEFAX: (216) 579-0212  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2040 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 178..1653  
; US-08-695-412B-11

Query Match 35.0%; Score 673.8; DB 2; Length 2040;  
Best Local Similarity 68.0%; Pred. No. 7.6e-196;

Matches 974; Conservative 0; Mismatches 447; Indels 12; Gaps 2;

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QY 166 tactttgatggaagcttatgatcaaaaccccttccacacagataaactaac 225
DB 268 TATTTTGTATGTTGGAAGCATATGATAGTATGCTTACCATTCCACCAGAAATCCTAAT 327
QY 226 ggtttatgcaaaatgggtcttgctgagaaatcagcttaacctgattgttggtgaagattgg 285
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DB 688 CAACCTCTTCCAAATGTTTGTGCGAGCTCCAATGATTTAAGGTCACTAAAGAATCCATG 747
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DB 1222 TTCACAAGAGGACTTGTCTCAAGTAGGCATTTGACACCTTAAAAAGCAGTGGCGGCTTTAT 1281
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## RESULT 4

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US-09-043-627-9
; Sequence 9, Application US/09043627
; Patent No. 6124525
; GENERAL INFORMATION:
; APPLICANT: Botella, Jose Ramon
; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MATHIJS, COLLINS, SHEPHERD & GOULD P.A.
; STREET: 100 Thonet Circle, Suite 306
; CITY: Princeton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08540-3662
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/043,627
; FILING DATE: 20-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU96/00591
; FILING DATE: 20-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN5559
; FILING DATE: 20-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN9603
; FILING DATE: 02-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernstein, Scott N.
; REGISTRATION NUMBER: 38,827
; REFERENCE/DOCKET NUMBER: 3573-11US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-924-8555
; TELEFAX: 609-924-3036
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1113 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1113
US-09-043-627-9

Query Match      33.0%; Score 635.2; DB 3; Length 1113;
Best Local Similarity 74.3%; Pred. No. 3.4e-184;
Matches 831; Conservative 0; Mismatches 278; Indels 9; Gaps 2;

QY 235 caaatgggtctgctgagatcagctaccctctgattggttggaagattggatactgaac 294
DB 1 CAGATGGGATTGGGGAAATCTGCTTTGCTTTGATTAGTTCAAGAATGGGCTTAAGC 60

QY 295 aaccctgaagcctccattgctaccctccaggaagaataaattgattccaggccatagctaac 354
DB 61 AACCCAGAGAAGCCCTATCTATCTGCACTGCCGAAGGTATAAGTGAATTTTCAGAGATATCGCTATC 120

QY 355 ttccaggattatcatggtctgcccaggttcagaaatgctggtctaaatttatggctaga 414
DB 121 TTTCAGGATTATCACGGCTTGGCAGAGTTTCAGAAATGCTGTTCGCAAAATTTTATGGCAAGA 180

QY 415 acaaggggaaacagatcaactgcttaccctgaccgctattgtctcatgagcgtgagccacc 474
DB 181 GTGAGAGGAATAGAGTCAATACGACCCTGATCGAATTTGTTATGAGCGGTGGAGCAACC 240

QY 475 gagacacagagtcactgctctttgtttggcagatccccggcgaggtcattcttagtgcgc 534
DB 241 GGAGCACATGAGACGGTGTGCTTTGCTTTGGCTGTATCCCGGTGAAGCATTTTGGGTGTC 300

QY 535 attccctattatccaggctttgaacgggattgagtgagacagaggttaaacctgtt 594
DB 301 ACTCCTTACTATCCAGGATTTGGTCAGATTTGAGATGGAGAACAGGAGTTCACATTTT 360

QY 595 ccagttatgctgagatgcataataatttcgtgttgacaaaaggaacattgggaagtgc 654
DB 361 CCAGTTGTGTGACAGTTCTAACATTTCAAGATTACAAGAGAACCGGTGGAAGCAGCA 420

QY 655 tatgagaagcagagagagataacatcagagtaagggtttactgatacccaatccatca 714
DB 421 TATGAAAAAGCTCAAGAAAGCACATCAGAAATCAAGGGTTTGGTCTCACAATCCATCG 480

QY 715 aatcattagccacatcatgacagaagacactgagacagcgtggtgaccttcatcaat 774
DB 481 ACCCGCTGGGACTTGTGTTGACAGAGAAACATAGAAGTTTGTAGTAAGCTTTCATTAAT 540

QY 775 gagaagcgtatccaccttgtatgtatgaataatctgctgcaacagttttca---gccaa 831
DB 541 GAAAGAACAATCCACTTAGTCTGCGAGAGATTATGCTGCCACATCTTCATGGGCCAG 600

QY 832 cccggtttcataagcatagctgagatattagaggatgaacagacatagagtgtgaccgc 891
DB 601 CCGGATTTTCATTAGCATCTCTGAAATTTATAGAAG-----AGATATTCACTGCAATCG 654

QY 892 aacctgctacacattggtttatagctcttcaaggacatagggttccctgacctcagagtc 951
DB 655 ATATCATCCACTCTGTTTACAGTCTTTCAAGAGATCTGGGGTTCCAGGCTTTAGGGTC 714

QY 952 ggcatacatactcttcaaatgatgctgtggttaattgtgcacgcaaaatgtcaagcttt 1011
DB 715 GGCATTATATACATACACAGATACAGTTGTGAGTTGGCGCTGCACAAATGTCAAGCTTT 774

QY 1012 gattggtgtcaacacagacagatcagttcttttagctatcgtatcgtataatgatgagttt 1071
DB 775 GCAGTTGTATATACACAAATCAACATTTAATGCTTCAATGTTATCAGATGATGAATTT 834

QY 1072 gtgagagattttctgcaagagtgcaagagtttggctcgaaggttcagggttttcaact 1131
DB 835 GTGATAGGTTCAATTAAGAGTGTCTAAAGGCTTTGCAAAAGGACAGAGGCTTTCA 894

QY 1132 ggggggttggccaaagtgtggcataaagtgtcttgcaagcaaatgctgtcttattgtgtg 1191
DB 895 TGGGGGCTATCTCAAGTAGGCTATGGTTGTTGAGAGAGCAATGCGGGGCTATTTTCTGG 954
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QY 1192 atgagatttaaggccaacttctcaaaaaagccaacttctgactctctgaaacggagcgtttgaaa 1251
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QY 1252 gttatcatcatgaagttaagatcaaatgttttccacctggctattccttccattgcactgag 1311
DB 1015 GTGATTAATCAACGAAGTTAAATTAATGTTTCTCCGGGTTCTTCCCTTTCATTGCGCTAAT 1074

QY 1312 ccagggtggtttagggtgctgctatgccaatggtatga 1349
DB 1075 CCAGGATGTTTCGGGTTGTTTCGCCAACATGGACGA 1112

RESULT 5
US-08-378-313-24
; Sequence 24, Application US/08378313
; Patent No. 6207881
; GENERAL INFORMATION:
; APPLICANT: THEOLOGIS, ATHANASIOS
; APPLICANT: SATO, TAKAHIDO
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,313
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29190-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 856-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2230 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..1545
US-08-378-313-24

Query Match      32.8%; Score 630.2; DB 4; Length 2230;
Best Local Similarity 65.4%; Pred. No. 1.7e-182;
Matches 961; Conservative 0; Mismatches 493; Indels 15; Gaps 2;

QY 51 acctttttacactccacactcttaaccacatacacatggttgcagggccatggacca 110
DB 54 AATTTCTTCACTTCTAACTCATTTTAGTAAAAAATGGGATTTGAGATTTGCAAGAC 113

QY 111 aactccctgttctcaagatggctattggggatggacatggcgaatcatccccatactt 170
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Db 114 CAACTCATCTTATCAAAATTTGGCTTACTAATGAAGAGCATGGCGAAAACTCGCCCATATTT 173  
Qy 171 t-gatgaggaagggcttatgatacaaaacccctttcatccacagataatcctcaacgggtg 230  
Db 174 TGATGGGTGGAAGCATACGATAGTATGATCTTTCCACCTCTAAAAACCCCAACGGAGT 233  
Qy 231 tatgcaaatgggtctctgtgagaaacagcttacctctctgatttgggtggaagtggatact 290  
Db 234 TATCCAAATGGGTCTTGTCTGAAATCAGCTTTGTTTAGACTTGATAGAGATTGGATTAA 293  
Qy 291 gaacaacctaaagccctcatttcactccagaaggaataaatgatattcaaggccatagc 350  
Db 294 GAGAAACCAAAAGGTTCAATTTG---TTCGAAGGAATCAATTCAGAGCCATTTGC 350  
Qy 351 taactttcaggattatcatggtctgcccagttcagaatgctggtggtctaaatttatggc 410  
Db 351 CAACCTTCAAGATTATCATGCTTGCCTGAATTCAGNNAACGATTCGCAAAATTTATGGA 410  
Qy 411 tagaacaaggggaacagaaataocgtttgcaacctgacccgtattgtcatagcggtygagc 470  
Db 411 GAAACAAAGAGGGAAGAGTTAGATTGTATCCAGAAAGAGTTGTATGTTGGTGTGC 470  
Qy 471 caccgagacacagcagtcactgcctctttgtttggcagatcccgcgaggcattcttagt 530  
Db 471 CACTGGACTAATGAGACAAATATATTTTGTGCTGATCCTGGCGATGCAATTTTATG 530  
Qy 531 gccctatccctattatccaggctttgaccggatttgaccggattgaggaacagagttaaaact 590  
Db 531 ACCTTCACCATACTACCCAGCATTTAACAGAGATTTAAGATGGAGAACTGGAGTACAACT 590  
Qy 591 tgttccagttatgctgtagctataaataattcgtgttgcaaaaggaagcattggaga 650  
Db 591 TATTCCAATTCACCTGAGAGTCGAAATTTTCAAAATTAATCTCAAAAGCAGTAAAAAGA 650  
Qy 651 tgccctatgagaaacagagaggataacatcagagctaaagggtttactgatcaccaatcc 710  
Db 651 AGCATATCAAAATGCAACAAATCAAAACATCAAACTAAAGTTTGCATTTTGACCCATCC 710  
Qy 711 atcaaatccattagggacaaatcatggacagaaagacactgagaaacggtggtgagcttcat 770  
Db 711 ATCAAAATCCATTTGGCACCACCTTTGGACAAAGACACACTGAAAGTGCTTTGAGTTTAC 770  
Qy 771 caatgagaagcgtatccacctgtgtgtagtgaataatactgtgcaacagttttcagca 830  
Db 771 CAACCAACACAAACATPCCACTTGTGTGTGACGNAATCTACGCGACCACTGCTTTGACAC 830  
Qy 831 acccggtttcataagcatagctlgagattatagaggatgaacacagacatagagttgacccg 890  
Db 831 GCCTCAATTCGTACATAGCTGAATCCTCGATGACACAGGAAATGACTTTACTGCAACAA 890  
Qy 891 caacctcglacacattgtttatagctcttcaagagacatg99gggtccctggcttcagagt 950  
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Qy 951 cggctatataactcttcaaatgactgctggtggttaattgtgcaacgcaaaatgtcaagctt 1010  
Db 951 CGGAATCATATATCTTTTAAACGAGATGCTGTTAATTTGCTAGAAAAATGTCGAGTT 1010  
Qy 1011 tggattggttcaacacagactcagatcttcttttagcatcgatcgaataatgatgatgagt 1070  
Db 1011 CGGTTTACTATCTACACAAACCATATATTTTTTACGGCAATGCTATCGGACGAAAAAT 1070  
Qy 1071 t9tg9agaggtttcttgcagagagtgcaaaaggtttggtctcaaaaggtttcagggttttcac 1130  
Db 1071 CGTCGATAATTTTCAAGAGAAAGCGCGATGAGGTTAGGTAAAGGCGCACAAACATTTTAC 1130  
Qy 1131 tggggggttgccaaagtgtgcataaaagtcttgcaaaagcaatgctgtgtctattgtgtg 1190  
Db 1131 TAATGGACTTGAAGTAGTGGGAATTAATAGCTTTGAAAAATTAATGCGGCGCTTTTGTGTG 1190  
Qy 1191 gatgatttaaggaactcttcaaaagcccaactctgactctgaacgagcgtttggaa 1250  
Db 1191 GATGGATTGGCTCCACTTTTAAAGGGAATCGACTTTTCGATACCGGAAATGTCGTTATGGAG 1250

Qy 1251 agttatcatcatgaagtttaagatcaatgtttcacctggctattcctccattgcactga 1310  
Db 1251 AGTTATATAAAGCATGTTAAGCTTAACGCTCGCTCGATCTTCGTTTGAATGTCAAGA 1310  
Qy 1311 gccagggtggttaggtgtgctatgccaacatgatgatgctggtgtgcaaatgtcttt 1370  
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Qy 1371 gcaacgaatccgcaactttgt-----gcttcaaaacaaggaggtcgtggtgc 1418  
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Qy 1419 taataagaaacattgtggcacagtaacttgaggtcagccctcaaaacaccagaggtttga 1478  
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Qy 1479 tgatatoccatgctcacctcacctctccc 1507  
Db 1491 TGAAGTGTGTTTGTCAACCACTTTTCGTCA 1519

RESULT 6  
US-07-809-457A-8  
; Sequence 8, Application US/07809457A  
; Patent No. 5512466  
; GENERAL INFORMATION:  
; APPLICANT: Klee, Harry J.  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: Control of Fruit Ripening and Senescence  
; TITLE OF INVENTION: in Plants  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Monsanto Co. B4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/809,457A  
; FILING DATE: 19911217  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,440  
; FILING DATE: 26-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner Jr., Dennis R.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10538)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1800 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
US-07-809-457A-8

Query Match 32.6%; Score 627; DB 1; Length 1800;  
Best Local Similarity 65.3%; Pred. No. 1.4e-181;  
Matches 959; Conservative 0; Mismatches 495; Indels 15; Gaps 2;  
Qy 51 acctttttacactccacactctaaacacacatacacatatggttttcaaggccatggacca 110

Db 117 AATTCTTCACTTCTAACTCATTTAGTAAAAAATGGATTTGAGATTTGCAAGAC 176  
QY 111 aactcccttggttccaaagatggctattggggatggacatggcgaatcatcccccactt 170  
Db 177 CAACTCAATCTTATCAAAATTTGGCTACTAATGAAGAGCATGGCGAAACCTCGCATATTT 236  
QY 171 tgaatgaagaagcttataatcaaaacccctttcccccacagataaatcctaaccgtgt 230  
Db 237 TGATGGTGGAAAGCATACCATAGTATCCTTTCCACCTCTAAAAACCCCAACGGAGT 296  
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QY 351 taactttcaggattatcatgctgctggccgagttcagaaatgctggtgtaaaattatgac 410  
Db 414 CAATTTCAAGATATATCATGCTTGCTGAATTCAGAAAAAGCATTCGGAATTTATGGA 473  
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Db 594 ACCTTCACCATACTACCCACATTTAACAGAGATTTAAGATGGAGAACTGGAGTACAACT 653  
QY 591 tgtccagttatgctgagatgctcaataatttcgtttgacaaaggaaagcattggaga 650  
Db 654 TATTCCAATTCACCTGTGAGAGCTCCAATATTTCAAAATTTACTTCAAAACGAGTAAAGA 713  
QY 651 tgcctatgaaagcgaagagagataacatcagagtaaaaggtttactatgcacccaatcc 710  
Db 714 AGCATATGAAATGCAAAAATCAACATCAAAATCAAAAGTAAAGTTGATTTTGACCAATCC 773  
QY 711 atcaatcattatgagacatcatgacagaaagacacactgagaccgttgtagcttcat 770  
Db 774 ATCAATCCATTTGGCCACCTTTGGCAAGACACACTGAAAAGTCTCTTGAGTTTCAC 833  
QY 771 caatgaaagcgtatccaccttgatgataatgataatgctgcaacagttttcagcca 830  
Db 834 CAACCAACACAACTCCACCTTTGTTGACGAAATCTACGAGCCACTGCTTTGACAC 893  
QY 831 acccggtttcacaagcatagctgagatattagaggatgaaacagacatagagtgtgaccg 890  
Db 894 GCCTCAATTCGTAGTATAGCTGAAATCCCTCGATGAACAGGAAATGACTTACTGCAACAA 953  
QY 891 caacctgctacacatggtttatagcttttcaaggacatgggttccctaggttccagagt 950  
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QY 951 cggcatcatactcttacaatgatgctggtggttaattgtgcacgcaaaaatgtcaagctt 1010  
Db 1014 CGAATCATATATCTTTAACGACGATGCTGTTAATTTGCTAGAAAAATGCGAGTTT 1073  
QY 1011 tggattggtgtcaacacagactcagtatcttttagcatcgatgtaaatgatgatgagt 1070  
Db 1074 CGGTTTAGTATCTACACAAACGCAATATTTTATGCGCAATGCCATCGGACGAAAAAT 1133  
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Db 1194 TAATGGACTTCAAGTAGTGGGAATTAATGCTTGAANAATTAATCGGGGCTTTTTGTTG 1253  
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Db 1254 GATGGATTTGCGTCCACTTTTAAAGGAATCGACTTTGATAGCGAANAATGCTTTATGGAG 1313  
QY 1251 agttatcatitcaagaatgaatcaatgtttccactggttatcttccatttgcactga 1310  
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RESULT 7  
US-08-553-943-8  
; Sequence 8, Application US/08553943  
; Patent No. 5702933  
; GENERAL INFORMATION:  
; APPLICANT: Klee, Harry J.  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: Control of Fruit Ripening and Senescence  
; TITLE OF INVENTION: in Plants  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Monsanto Co. B84F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,943  
; FILING DATE: 06-NOV-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/809,457  
; FILING DATE: 17-DEC-1991  
; APPLICATION NUMBER: US 07/632,440  
; FILING DATE: 26-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner Jr., Dennis R.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10538)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1800 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
US-08-553-943-8

Query Match 32.6%; Score 627; DB 1; Length 1800;  
Best Local Similarity 65.3%; Pred. No. 1.4e-181;  
Matches 959; Conservative 0; Mismatches 495; Indels 15; Gaps 2;

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QY 51 acttttttacactccacacttaacacacatacacacataatgaggtttcaaggccatggacca 110
DB 117 AATTTCTTCACCTCTTAAACTCATTTAGTAAATAAATAAATAAATAAATAAATAAATAA 176
QY 111 aactcccttgggtccaaagatggctattgggtgagatggagatgacatgcaatcatcccatatt 170
DB 177 CAACTCAATCTTATCAAAATGGCTTACTTAATGAAGAGCATGCGGAAAACCTCGCCATATTT 236
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DB 237 TGATGGGTGGAAGCATACGATAGTATCTTTCCACCTCTTAAATAAACCCTCAACGGAGT 296
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DB 297 TATCCAAATGGGTCTTGTCTGAAATTCAGCTTTGTTTAGACTTGATAGAAGATTGGATTAA 356
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DB 594 ACCTTCCACCATATACCCAGCATTTTAAACAGAGATTAAAGATGGAGAACTGGAGTACAACT 653
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DB 654 TATTCCAATTCACGTGAGAGCTCAATTAATTTCAAAATTTACTTCAAAAGCAGTAAAGA 713
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DB 714 AGCATATGAAATGCACAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAAA 773
QY 711 atcaaatccattaggacaaatcatgagacaaagacactgagaaacgtggtgagcttcatt 770
DB 774 ATCAATCCATTGGGCACCACTTTGGACAAAGACACACTGAAAGATGCTTTGAGTTTCAC 833
QY 771 caatgagagcgtatccacttggatgagatgaaatataatctgcaacagattttcagcca 830
DB 834 CAACCAACACAACTCCACCTTGTGTGTGAGCAAAATCTACGACGCACTGCTTTTGACAC 893
QY 831 acccggtttcataagcaagctgagatattagagatgaaacagacatagaggtgtgacgg 890
DB 894 GCCTCAATTCGATATAGTGAATCTCGATGAACAGGAAATGACTTACTGCAACAA 953
QY 891 caactctgacacattgtttatgctttcaaggacatgggggttccctggcttcagagt 950
DB 954 AGATTTAGTTTACATCGCTCAGCTTTTCAAAAGACATGGGTTTACCAGGATTTAGAGT 1013
QY 951 cggatcatatctctacatgatgctgtgttaattgtacagcaaaatgtcaagctt 1010
DB 1014 CGGAATCATATATCTTTTACGAGAGTGTCTGTTAAATTTGCTGATAAATAATGTCGAGTTT 1073
QY 1011 tggattggtgacacacagactcagatcttttttagcatcgatcgatctaaatgatgagtt 1070
DB 1074 CGGTTTAGTACTACACAAACGAATATTTTTTAGCGCAATGCCATCGGACGAAATAAT 1133
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QY 1071 tgtgagaggttttctggtgagagagtgcaagaggttggctcaaggttcagggttttccac 1130
DB 1134 CGTCGATAATTTTCTAAGAGAAAGCGGATGAGGTAGGTAAAGGCAACAACATTTTAC 1193
QY 1131 tgggggggttggccaaagtgtgataaaagtgttgcacaaagcaatgtggtctctattgtgtg 1190
DB 1194 TAATGGACTTGAAGTAGTGGGAATTAATGCTTGAATAAATAATGCGGGCTTTTGTGTG 1253
QY 1191 gatgatttaaggcaactcttcaaaagcgaactttcgactctgaacgagagcttttggaa 1250
DB 1254 GATGATTGCTGCCACTTTTAAAGGAATCGACTTTGATAGCGAAATGCGTTATGGAG 1313
QY 1251 agttatcatctaatgaattgaatcaatgtttcacctggctattcttccattgcactga 1310
DB 1314 ACTTATATAAAGCATGTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAA 1373
QY 1311 gccaggggttgggttgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1370
DB 1374 GCGAGGTGGTTCGAGTGTGTTTGAATAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1433
QY 1371 gcaacgaatccgcaactttgt-----gcttcaaaacaaaggaggtcgtggtgc 1418
DB 1434 CCGAGGATTCGAGGTTGCTAGGTGTGAGAAAGTGGAGATAAATCGAGTTCGATGA 1493
QY 1419 taataagaaacattgttgcacagtaacttggaggtgagcctcaaaacacagaggtttga 1478
DB 1494 AAGAAGCAACAATGGAAGCAATAATTTGAGACTTAGTTTTCGAAAAAGAAATGATATCA 1553
QY 1479 tgatataccatgctcacctcactctccc 1507
DB 1554 TGAAAGTGTGTTGTCCACCACCTTTTCGTCAC 1582
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RESULT 8  
PCT-US91-09437-8  
; Sequence 8, Application PC/TUS9109437  
; GENERAL INFORMATION:  
; APPLICANT: Klee, Harry J.  
; APPLICANT: Kishore, Ganesh M.  
; TITLE OF INVENTION: Control of Fruit Ripening and Senescence  
; TITLE OF INVENTION: in Plants  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Monsanto Co. B4F  
; STREET: 700 Chesterfield Village Parkway  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US91/09437  
; FILING DATE: 19911217  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,440  
; FILING DATE: 26-DEC-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hoerner Jr., Dennis R.  
; REGISTRATION NUMBER: 30,914  
; REFERENCE/DOCKET NUMBER: 38-21(10538)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6099  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1800 base pairs  
; TYPE: NUCLEIC ACID

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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
PCT-US91-09437-8

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Query Match 32.6%; Score 627; DB 5; Length 1800;  
Best Local Similarity 65.3%; Pred. No. 1.4e-181;  
Matches 959; Conservative 0; Mismatches 495; Indels 15; Gaps 2;

QY	51	acttttttacactccacactctaaocacatacacccatatggggtttccaaggccatggacca	111
DB	117	AAATTTCTTCACTTCTAAACTCATTTAGTAAAAAATAATGGGATTTGAGATTTGCAAGAC	176
QY	111	aactcccttggtgccaaagatggctatggggatggacatggcgaatacatccccatactt	170
DB	177	CAACTCAATCTTATCAAAATTTGCTACTAATGAAGAGCATGCGAANAACCTGCCATATTT	236
QY	171	tgatgatggaagcgttatgatcaaaacccctttcatccacagataatcctaaacggtgt	230
DB	237	TGATGGTGGGAAGCATACGATAGTCATCTTCCACCTCTAAAAAACCACACGGAGT	296
QY	231	tatgcaaatgggtcttgctgagaaatgaagcttacctctctgattggttgaaagattgatact	290
DB	297	TATCCAAATGGGTCTTGCCTCAAAATCAGCTTTGTTTATAGACTTGATAGAAGATTGGATTAA	356
QY	291	gaacaacctgaagctccatttgcactccagaagaataaaatgatttcaaggccatagc	350
DB	357	GAGAAACCCAAAGGTTCAATTTG--TTCCTGAAGGAATCAAAATCATTTCAAGGCCATTTGC	413
QY	351	taactttcaggattatcatggtctggccgagcttcagaaatgctgtggctaaatttatggc	410
DB	414	CAACTTCAAGATTATCATGGCTTGCCCTGAATTCAGAAAAGCGATTGCGAAATTTATGGA	473
QY	411	tagaacaaggggaacagaaatcacgtttgacctgacctgacogtattgtcatgagcgtggagc	470
DB	474	GAAAAACAAGAGGAGGAAGATTAGATTTTGATCCAGAAAGAGTTGTTATGCTGGTGGTNGC	533
QY	471	caccgagcacagcagtcactgcctttgtttgttgcaatccccgcgagcagctcttagt	530
DB	534	CATCGAGCTATGAGACAATTTATATTTTGTGTGCTGATCCTGCGGATGATTTTATGT	593
QY	531	gccattccctattatccaggctttgacgggatttgacggttgagggtggagaaacaggagttaaact	590
DB	594	ACCTTCACCATACTACCCAGCATTTAACAGAGATTTAAGATGGAGAACTGGAGTACAACT	653
QY	591	tgttcagttatgcgatagctcaataattctdgttgcaaaaggaagcattggaaga	650
DB	654	TATTCOAATTCATGTGAGAGCTCCAATAATTTCAAAATTTACTTCAAAAGCAGTAAAAAGA	713
QY	651	tgctatgagaagcaagagagataaactcagatgaaggtttactgatacccaatcc	710
DB	714	AGCATATGAANTGCAAAAATCAACATCAAACTAAAGTTTGAATTTTGACCAATCC	773
QY	711	ataaatccattaggcacatactggacagaagacactgagaaacggtggtagcttcat	770
DB	774	ATCAAAATCCATTGGGCACCACCTTGGACAAAGACACACTGAAAAGTGTCTTGAGTTTCAAC	833
QY	771	caaagagaagcgtatccacctgtatgtatgaaatatactgtcaacagttttcaogcca	830
DB	834	CAACAAACAACAATCCACCTTGTGTGTGACGAAATCTACGACGCCACTGTCTTTTGACAC	893
QY	831	acccggtttcaagcatagctgaatatagagatatgaacagacatatagatgtgaccg	890
DB	894	GCCTCAATTCGGTATAGCTTGAATCCTCGATGAACAGGAATGACTTTACTGCAACAA	953
QY	891	caacctcgtcacactgtttagtcttttcaaagacatgggttccctggcttcagagt	950
DB	954	AGATTAGTTCACATCGTCTACAGTCTTCAAAAAGACATGGGTTTACCAGGATTTAGAGT	1013
QY	951	cggcatcatatactcttacaatgatgctgtggttaattgtgaocgcaaaatgtcaagett	1010
DB	1014	CGAAATCATATATCTTTTAAACGACGATGCTGTTAATTTGCTAGAAAAATGTCAGTTT	1073

Qy	1011	tgattggtgtgcacacagactcagtatctttagctatcgatgctaaatgatgatgagtt	1077
Db	1074	CGGTTTAGTATCTACACAAACCAATATTTTTTAGCGCAATGCCATCGGACGAAAAATT	1133
Qy	1071	tgtggagaggtttctgcagagagtgcaaaaggttgctcaaagttcagggtttttcac	1130
Db	1134	CGTCGATAATATTTCTTAAGAAAGCCGATGAGTTAGGTAAAAGGCACAAACATTTTAC	1193
Qy	1131	tgggggggttggccaaagtgtgcataaagtgcctgcaaaagcaatgctggctctatttgtg	1190
Db	1194	TAATGGACTTGAAGTAGTGGGAATTAATGCTTGAAAAATAATCGGGGCTTTTTTGTG	1253
Qy	1191	gatgatttaaggcaactctctcaaaagcccaacttgcactctgaaacggagcttggaa	1250
Db	1254	GATGGATTTCGCGCCACTTTTAAGGGAATCGACTTTTCGATAGCGAAATGTCGTTATGGAG	1313
Qy	1251	agttatactcatgaagttaagatcaatgtttccactggctatctctccatgcactga	1310
Db	1314	AGTTATTATAACGATGTTAAGCTTAACGTCGCTTGGATCTCGTTTGAATGCTCAAGA	1373
Qy	1311	gccagggtggttagtggtgtgatgccacaatgatggtctgtgcgaattgcttt	1370
Db	1374	GCCAGGGTGTTCGGAGTTGTTTTCGAAATATGCGATGATGGAACGGTTGATATTGCGCT	1433
Qy	1371	gcaacgaatccgcaactttgt-----gcttcaaaccaagagagctcgtggtgctc	1418
Db	1434	CGCGAGGATTCGGAGTTCGTAGGTGTTGAGAAAAAGTGGAGATAAATCGAGTTCGATCGA	1493
Qy	1419	taataagaacaatgttgcacagtaacttgagctgagctcctcaaacagaggtttga	1478
Db	1494	AAGAAGCAACAATGGAAGAACAAATAATTTGAGACTTGTAGCTTTTCGAAAAGAATGTATGA	1553
Qy	1479	tgatataccactgtcacctcactctcccc	1507
Db	1554	TGAAAGTGTTTGTGCACCACCTTTGCTGCAC	1582

RESULT 9

US-08-724-194-2

Sequence 2, Application US/08724194

Patent No. 5824875

GENERAL INFORMATION:

APPLICANT: RANU, RAJINDER S.

TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE

TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE

TITLE OF INVENTION: IN GERANIUMS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: SANTANGELO LAW OFFICES PC

STREET: 315 WEST OAK STREET, STE 701

CITY: FORT COLLINS

STATE: CO

COUNTRY: USA

ZIP: 80521

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,194

FILING DATE: 01-OCT-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: SANTANGELO, LUKE

REGISTRATION NUMBER: 31,997

TELECOMMUNICATION INFORMATION:

TELEPHONE: (970) 224-3100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2678 base pairs

TYPE: nucleic acid

## RESULT

US-08-724-194-2  
Sequence 2, Application US/08724194  
Patent No. 5824875  
GENERAL INFORMATION:  
APPLICANT: RANU, RAJINDER S.  
TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE  
TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS  
TITLE OF INVENTION: IN GERANIUMS  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SANTANGELO LAW OFFICES PC  
STREET: 315 WEST OAK STREET, STE 701  
CITY: FORT COLLINS  
STATE: CO  
COUNTRY: USA  
ZIP: 80521  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,194  
FILING DATE: 01-OCT-1996  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: SANTANGELO, LUKE  
REGISTRATION NUMBER: 31,997  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (970) 224-3100  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2678 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-724-194-2

Query Match 32.6%; Score 627; DB 1; Length 2678;  
Best Local Similarity 66.6%; Pred. No. 1.8e-181;  
Matches 913; Conservative 0; Mismatches 455; Indels 3; Gaps 1;

QY 122 tgcacaagatggtctattggggatggacatggcgaaatcatcccccatactttgatgatga 181  
DB 64 TGTCAAGAGATTCCACCAACGACGACGACGCGGCAACTCCCCATATTTTCGATGGTTGA 123  
QY 182 aggtctatgatcaaaacccctttccacacagataaactcaacaggtgttatgcaaatgg 241  
DB 124 AGGCTTATGACCGTATCGTTCCATCGTCTCAGAAATCCTAACGGTGTATCCAGATGG 183  
QY 242 gcttgcgtgagatcagcttacctctgtattgttgaagattggatatactgaacaaccttg 301  
DB 184 GTTTAGCTGAANAATCAGCTTTTCATCTGACTTCTGATTGTAAGATTGGGTAGGTCACCCAG 243  
QY 302 aagctccaatcttgctccacaggaagaaataaatgatttcaggggccatagctaaacttcagg 361  
DB 244 AAGCCTCAATCTGCATCTAGAGGAGTGGTAAGTTCAAGGACGTAGTAATCTTCAGG 303  
QY 362 attatcatggttgcgcaggttcagaaatctgtgtgcttaaaatttatgctagaaacaagg 421  
DB 304 ACTAGCATGGCTGTGTGGAGTTTCAGGACGCGCGTGGCTAAATTTATGACGAGGAAGGG 363  
QY 422 gaaacagaatcagtttgacctgacctgattgtatgagcggttgagccaccggagcac 481  
DB 364 GCGGAAGGTCAATTTGATCCGACCGGTGTCTGATGAGCGGCGGACCGGAGGCA 423  
QY 482 acgaagtcactgctttgtttggcagatcccgcgaggtcttcttagtgccttccct 541  
DB 424 ACGAGCTCATCTCTCTGTTTGGCAATCCCGGAGCGCTTCTCTTCCCATCTCCTT 483  
QY 542 attatcaggttgcgcaggttgcagaaatctgtgtgcttaaaatttatgctagaaacaagg 601  
DB 484 ATTATCCAGGAACGACGCTGACTTGCATGGCGGCAACGCGGACTCAGATCATTCGGGTG 543  
QY 602 tctgcgagatcgaataatttcgtgtgacaaagagcattggaagatgcttatgaga 661  
DB 544 ACTGCAACAGCTTCCACGGTTTCAAGATTAACCAAGAGAGCCCTAGAAGATCATCGCAC 603  
QY 662 aagcaagagaggaataacatcagatgaaaggggtttactgatcaccacatccatcaaatccat 721  
DB 604 AAGCAACAAGAAAGCAACATAAAGCTAAAGGGGTGCTCTTAACCAACCATCGAACCCCTC 663  
QY 722 taggcacaatcctgacacagaaagacactgagaaacctggtgagcttcatcaatgagaagc 781  
DB 664 TAGGCACAATTTGGACCGCGACACTCTCAAGAGCATGCTCAGCTTCGTCACCGACAACA 723  
QY 782 gtatccacctgtatgtatgaaatatactgtgcacaggttttcagccacccgggtttca 841  
DB 724 ACATCCACTAGTATCGACGAATTTCTAGCGCGCCACCGTTTTTCGCCGCCCGGAGTTCG 783  
QY 842 taagcatagctgagatatttagaggatgaacacagacatagagtgtgaccgcgaacctcgtac 901  
DB 784 TAAGCGTCTCCGAATCTCCAAAGAAATGAGACGACACCCACGTCGCAACCCGACCTCATCC 843  
QY 902 acatgtttatagtttccaaggacatgggggttccctggcttcagagtcgagtcgcatcat 961  
DB 844 ACATCGTGTACAGCCTGTCCAAGGACTTGGGCATGCGCGGGTTCCGCGTTCGGGATCGGT 903  
QY 962 actctacaatgatctgtgtggttaattgtgcacgcaaaatgtcaagcttttgattgggtgt 1021  
DB 904 ACTCATTCACCGACGCTGCTGTTCTCTGCGCACGGAAGATGTCGAGCTTCGGGGTGGTGT 963  
QY 1022 caacacagactcagttatcttttagcatgattgcttaaaatgattgattgttggagaggt 1081  
DB 964 CGACCCAGACGCGACACCTTCTTCGACGCGATGCTATCCGACGACCGCTTTCGTGGAGCGGT 1023

QY 1082 ttctgacagagagtgcacaagaggttggctcaaggttcagggttttcaactgggggttgg 1141  
DB 1024 TCCTCGCGGAGAG---CCGGAGCTTGGGGAGGAGGCACGGCTGTTTCACGAAAGGCTCG 1080  
QY 1142 ccaaaagtgtgcataaaagtgtcttgcaaaagcaaatgctgggtctatttgtgtgagtgattaa 1201  
DB 1081 AGGAGTGTGGGATGTGGTGTAAAGAGCAACGCGGGCTACTTCTGGATGGATTTGC 1140  
QY 1202 ggcacttctcaaaagcacaactttcactctgaaacgagccttggaaagtattacatic 1261  
DB 1141 GGAAGCTTCTAGAAAGACAGACCTTTGAGCGGAGATGCTGTGGAAAGGTGATTATTA 1200  
QY 1262 atgaagtttaagtcaatgtttcacctggctatttcttccattgctgcaactgagccaggtgtgt 1321  
DB 1201 ATGAGGTGAAGCTAAACGCTCTCGGGGTCTCGTTCGTTTCATTTCGTGGAGCGGGTGTGT 1260  
QY 1322 tttaggtgtctatcccaacatggtatgatatggtgtgcaaatgttcttgcgaacgaatcc 1381  
DB 1261 TTAGGGTTTGTTCCTCCACATGGACGAGACGCTCCACGTGGCGCTGAAGAGGATCA 1320  
QY 1382 gcaactttgtgtctcaaaacaaagaggtcggtgtgtcttaataagaacacattgttgccaca 1441  
DB 1321 GGGCGTTGTGGGGAAGAGAGGTGGGTCCGCTGAAGAGGAGAGGTTTCATGGACAACC 1380  
QY 1442 gtaactgaggtcgagctcaaaacaaagaggttggattgattgatcatcaccatgt 1492  
DB 1381 TTAACCTCAGGCTGAGCTTCTCGTCTAAGGTAGGTAGAGTGTGATGT 1431

RESULT 10  
US-08-724-194-1  
; Sequence 1, Application US/08724194  
; Patent No. 5824875  
; GENERAL INFORMATION:  
; APPLICANT: RANU, RAJINDER S.  
; TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE  
; TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: SANTANGELO LAW OFFICES PC  
; STREET: 315 WEST OAK STREET, STE 701  
; CITY: FORT COLLINS  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80521  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,194  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANTANGELO, LUKE  
; REGISTRATION NUMBER: 31,997  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (970) 224-3100  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1945 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-724-194-1

Query Match 32.5%; Score 625.4; DB 1; Length 1945;  
Best Local Similarity 66.5%; Pred. No. 4.6e-181;



Matches 854; Conservative 0; Mismatches 426; Indels 6; Gaps 1;			
Qy	122	tgtccaagatggtctattggggatgacatgagcaatcaccatccttcttgatgatga	181
Db	51	TCTCGAAGATCGCCCTCGACGATGCGCGAGAACTCCCGGTATTTCGATGGTGA	110
Qy	182	aggtctatgatcaaaaccccttctatccacacagataactcaacggtgttatacgaatgg	241
Db	111	AAGCTTACGATACCAATCCGTTTACCCCTGAGAAATAATCCTTTGGGTGTATTCAATGG	170
Qy	242	gtctgtcagagatcagcttacctctgattgttggttgagattggagatactgaacaacctg	301
Db	171	GTTTAGCAGAAAATCAGCTTTCTTTGATATGATTGTAGCTGGATTAGAAAACCCCTG	230
Qy	302	agacctccatttgcactccagagaagaataaattgattcaggcccatagctaactttcagg	361
Db	231	NAGCTTCGATTTGTACACCGAAGGACTTGAGAGATTCAAAAGCATTGCCAACTTCCRAAG	290
Qy	362	attatacagttgtggtccgagttcagaatgctgtgtgctaaatttatgctagaaacagg	421
Db	291	ATTACCACGGCTTACAGAGTTTCGAAATGCAATTTGCAAAATTTATGGGGAAGTAAGAG	350
Qy	422	gaacagaaatcagtttgaacctgacctgattgtctatgagcgttgagaccacccgagcac	481
Db	351	GTGGGAGGTAAATTCGACCCGAGTCGGATTGCTATGGTGGCGGTGGACCGGAGGA	410
Qy	482	acgaagtcaactccctttgtttggcagatcccgcgagggcattcttagtgcacattccct	541
Db	411	CGGAAACCGTCATCTTTTGTGGCGGATCCGGGGATGCTTTTTTGGTTCTCTCCAT	470
Qy	542	attatccaggtttgacccgggtttgaggtgagaaacaggaagttaaaactgttccagtta	601
Db	471	ATTATGACAGGATTTGATCGAGACTTGAATGGCGAACACGACGACCAATAATTCGGGTCC	530
Qy	602	tgtcgtatagctcaaatcttcgttgtagaagaagcattggaagatgctctatgaga	661
Db	531	ATTGCAACGGCTCGAATAACTTCCAACTCACAAGCGACCTTAGAATAATGAGCTACAAA	590
Qy	662	aagcaagagaggataacatcagatgaagggtttactgatacccaatccatcaaatccat	721
Db	591	AGGCTCAAGAGGCCAACATGAAGTGAAGGTGTTAATAATCACCAATCCCTCAAAATCCCT	650
Qy	722	taggcacaatcattgagacagaagacacatgagaaacccgtgtgagcttcaatcagagac	781
Db	651	TAGGCACAACGTPACGACCGTGACATCTTAAACCCCTCGTCACCTTTGTGAATCAACACG	710
Qy	782	glatccaccttgtatgtatgaatatatgtgtcaacagttttcagccaacccggtttica	841
Db	711	ACATTCACTTAATATGCGATGAATATACTCTGCCACTGTCTTCAAGCCCCCAACCTTCA	770
Qy	842	taagcatagctgagatatatagaggatgaacagacatagagtgtgacccgcaacctcgtac	901
Db	771	CCAGCATCGCTGAGATTGT- ----TGAACAAATGGAGCATTGCAAGAAGGAGCTCATCC	824
Qy	902	acattgtttatagttttcaaggacatgggtttccctggcttcagatcgccgcatcatat	961
Db	825	ATATTCTTATAGTGTGCCAAGACATGGGCTCCCTCGTGTTCGAGTTTGAATTAATTT	884
Qy	962	actcttacaatgactgctgtgtgttaattgtgacgcgaataatgtcaagctttgtggtgtg	1021
Db	885	ATTCTTACAAACGATGCTGCTGCTCGCCGCTGCTCGGCAGATGTCGAGCTTCGGCCTCGTCT	944
Qy	1022	caacacagactcagtatcttttttagcatcgatgctgtaaaatgatgatgatttgtgagaggt	1081
Db	945	CGTCCAGACTCAACATTTGCTCGCGGCATGCTTTCCGACGAGGACTTTTGTGCAAAAT	1004
Qy	1082	tcttcgacagagatgcaagaggttggctcaaaagtttcagggttttctactgggggttgg	1141
Db	1005	TTCTTGGCGAGAACTCGAAGCGTGTGGCGAGAGGATGCAAGGTTCAAAAAGAAATTTGG	1064
Qy	1142	ccaaagtgtgcaataaagtgtgcaaaagcaatgctgggtctctatttgtgtgagtggaattaa	1201
Db	1065	ATAAAATGGGGATCACTTCTTTGAACACGCAATGCTGGAGTTTGTGTGGATGGATCTAC	1124

Qy	1202	ggcaacttctcaaaaagccaaactttcgaactctgaaacgagactttggaaaagtatacttc	1261
Db	1125	GGAGGCTATTAAAGACCAAAACCTTCAAAGCTGAAATGGAGCTTTGGCGTGTGATTATCA	1184
Qy	1262	atgaagtttaagatcaaatgtttcacctggctatctctccatctgcactgagccaggtggt	1321
Db	1185	ATGAAGTCAAGTCAATGTCTCTCGCTCATCTCTTTCATCTCAGCCAGGTTGGT	1244
Qy	1322	ttaggtgtgctatcccaactgagatgatgtgctgcaaatgtcttttgcacgaactcc	1381
Db	1245	TTGAGTTTGTTCGAAACATGGAGACACACCGTTGACGTTGCTCTCTCAATAGAAATCC	1304
Qy	1382	gcaactttgtgcttcaaaaacaaaggag	1407
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RESULT 12  
US-08-632-598-1  
; Sequence 1, Application US/08632598  
; Patent No. 5886164  
; GENERAL INFORMATION:  
; APPLICANT: BIRD, COLIN R  
; APPLICANT: FLETCHER, JONATHON D  
; TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY AND CUSHMAN  
; STREET: 1100 NEW YORK AVENUE N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/632,598  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 223355/SPE50112/US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 861-3000  
; TELEFAX: 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1712 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; ORIGINAL SOURCE:  
; ORGANISM: MUSA  
; IMMEDIATE SOURCE:  
; CLONE: ACS GENE  
US-08-632-598-1

Query Match 29.7%; Score 571.4; DB 2; Length 1712;			
Best Local Similarity 64.1%; Pred. No. 1.3e-164;			
Matches 914; Conservative 0; Mismatches 501; Indels 12; Gaps 3;			
Qy	122	tgtccaagatggtctattggggatgacatgagcaatcaccatccttcttgatgatga	181
Db	62	TCTCTCGATCGCGACCAACGACGCCCATGCGGAGAACTCCTCTACTTCGATGCTGGA	121



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QY 182 aggttatgatcaaaaccccttccatccccacagataataactaaacgggtgttatgcaaatgg 241
Db 122 AGGCTTACGAGAGAGATCCCTTTCCACCTCACCGCAACCCACGCGGGTTCATCCAAATGG 181
QY 242 gtctgtgagaaacagcttacctctctgattggttgaagattgataactgaacaacctg 301
Db 182 GACTCGCAGAAACCAGCTTTCCCTCGACTTGATCCGAGACTGGATGAAGAAGAACCCAC 241
QY 302 aagctccatttgcaactccagaggaataaattgatttcaggccatagctaaacttcagg 361
Db 242 AGGCTTCGATCTGCACCGCAAGAGAGGGTCTCAGAGTTTCAAAGCAATTTGCCAACTTTCAGG 301
QY 362 attatcatgtctgcccaggttcagaataactgtggtgataattatgctagaaacagg 421
Db 302 ACTATCATGCGCTCCCAACCTTTCCGAAGGCCATCGGCCCGCTTCATGGAGAAAGGTGAGAG 361
QY 422 gaaacagaatacacgtttgacccctgacccgtattgtcatgagcgggtgagccacccggagcac 481
Db 362 GGGACGAGCCAGATTTTACCCAGACCGCATCGTGATGAGCGGTGGAGCCACCGCGGCTC 421
QY 482 acgaagtcaactgtttgttggcagatccccggcgagggtattcttagtgcccaattccct 541
Db 422 AGGAACCATCGCCCTTTTGGCTGGCTGATCTTGGCGAGGCGCTTCTTGATTCCAAACGCAT 481
QY 542 attatccagctttgacgggatttgaggtggagacagaggttaaaacttgttccactta 601
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QY 602 tgtgcatagctcaataattctgtgtgacaaaggaagcattggaagatgcctcatgaga 661
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QY 662 aagcaagagaggataaatacatcagagtaaggggtttactgtatcaccaatccatcaaatccat 721
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QY 722 taggcaaatcatgacagaaagacacatgagaacccgtggtgagcttcatcaatgagaagc 781
Db 662 TGGCAACACCATGGAGCAGAGACGCTGAGAACCCCTAGTCAGCTTCGTCAACAGAGAAAA 721
QY 782 gtatccacctgtatgtatgataataatctgctgaacagttttcagccaacccggtttca 841
Db 722 GGATGCACCTTGGTGGAGCAGATCTTCTCCGAACCGTCTTCGACAGCCGAGTTACG 781
QY 842 taagcatagctgagatattagagatgaaacagacataagagtgtgacccgaacctgtac 901
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QY 902 acattgtttatagctcttcaagagacatgggttccctggtcttcagagtgcgcatcatat 961
Db 836 ACATCGGCTACAGCCTCTCCAAGGACCTGGCGCTGCCCTGGCTTCGCGTCCGGCTCATAT 895
QY 962 acttataaatgatgtgtgttgaattgtgcaacgcaaaatgcaagcttttgattgtgt 1021
Db 896 ACTCTTACACGAGCGCGTGTGAGCTGCGGAGGAGAGATGTCAGGCTTTGGACTGTCT 955
QY 1022 caacacagactcagatctcttttagctatcgatgctaaatgatgatgtgtgtgagaggt 1081
Db 956 CGTGCAGACGCGACTCTCTGCTGCTTCCATGTTGGGAGACGAGGAGTTTCAACACGAGTT 1015
QY 1082 ttctggcagagagtcaaaaggttggctcaaggttcagggttttcaactggggggttgg 1141
Db 1016 TCTTAGCGAGCGAGCGGACGAGGTTGTGCGGGCGGCGCAGGGTCTTTACGAGCGGCTCA 1075
QY 1142 ccaagttggcataaagtgtctgcaaaagcaatgctgtgtctatttgtgtgattgatttaa 1201
Db 1076 AGCGAGTCGGGATTCATTGCTTGGACCGCAACCGCGGGGCTGTTCTGCTGATGACACTTGA 1135
QY 1202 ggcaactctcaaaagcaacttccgactctgaaacggagccttggaaaggttatcttc 1261
Db 1136 GGCGGTGCTGAGGAAGACGACGGTGGAGCGGACGCTCCGCTGTGCGGGGTGATCATCA 1195
QY 1262 atgaagttaagatacaatgtttccactggctatttccctccattgcaactgagccagggtggt 1321
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Db 1196 ACGACGTGAAGCTCAACATCTCGCGGGGTGCTCTTCCACTGCTCGAGCCGGGTGGT 1255
QY 1322 ttagggtgtgctatgccaacatggatgatgtggtgtgcaaatgtcttgaacgaatcc 1381
Db 1256 TCAGGGTGTGCTTCGCCCAACATGGACACAGCGGCCATGAAGATAGCGCTGAGGAGGATCG 1315
QY 1382 gcaactttgtg---cttcaaaacaagagggtcgtgtgtcttaataaagaacatgttggc 1438
Db 1316 AGATTTCGTGTACCGGAGAACGACGCGCTGTGCAAGCGCAAGAACAGAGAGGTGGG 1375
QY 1439 acagtaactgaggtgagcctcaaaacacagaggtttgatgat---atcaccatgtcac 1495
Db 1376 ACGAAGCGCTGCGGCTGAGCTTGCTCGTGGAGGTTGCGAGGATCCGTCCATCATGACAC 1435
QY 1496 ctcaactctccctcactcagtcacactatggtttaaagccacacaaatga 1542
Db 1436 CACATCTGATGTCTCTCCACCATCGCCTCTCGTTCAAGCCGCCACCTGA 1482

RESULT 13
US-09-231-240-1
; Sequence 1, Application US/09231240
; Patent No. 6262346
; GENERAL INFORMATION:
; APPLICANT: BIRD, COLIN R
; APPLICANT: FLETCHER, JONATHAN D
; TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY AND CUSHMAN
; STREET: 1100 NEW YORK AVENUE N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,240
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,598
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 223355/SEE50112/US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 861-3000
; TELEFAX: 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1712 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: MUSA
; IMMEDIATE SOURCE:
; CLONE: ACS GENE
; US-09-231-240-1

Query Match 29.7%; Score 571.4; DB 4; Length 1712;
Best Local Similarity 64.1%; Pred. No. 1.3e-164;
Matches 914; Conservative 0; Mismatches 501; Indels 12; Gaps 3;
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NAME/KEY: CDS  
LOCATION: 1..1104  
US-09-043-627-3

Query Match 29.7%; Score 571.2; DB 3; Length 1104;  
Best Local Similarity 71.6%; Pred. No. 1.2e-164;  
Matches 792; Conservative 0; Mismatches 308; Indels 6; Gaps 3;

QY 235 caaatgggttctgtgagatcagcttaccctctgatttggttaagattgatactgaac 294  
DB 1 CAGATGGCCCTTGTGAGATCAGCTTGTCTTAATTAATTCACGAGTGGCCGCTGAAA 60

QY 295 aacctgaagcctccatttcacccagaagggaataaatttcaggggccatagctaac 354  
DB 61 AACCCAGAGCCCTCATTTGTACACACAAAGGAGCAGCTGAATTCAGAGATATAGCTATC 120

QY 355 ttccaggtattcatgtctgtgcccagcttcagaaatcgttgctaaatttatggctaga 414  
DB 121 TTTCAAGATTATCATGCTTGGCTGTAATTCAGAGAGCTGTTCGAAAGTTATGGGAAA 180

QY 415 acaaggggaacagaatcacgtttgaccctgacccgtattgtcatgagcgtggagccacc 474  
DB 181 GTGAGAAGAACACAGAGCTTCTATTACCCCTGATCGGATTTGTATGAGTGGAGGAGCACT 240

QY 475 ggagcacagaagtcactgcctttgtttggcagatccccggcaggcattcttagtgccc 534  
DB 241 GGAGCTCATGAAATGATGTGTTTCTGTGTGGCTGATCCTGGCGATGCAATTTGGTTCCA 300

QY 535 atccctattcatcagcgtttgacccggtattgagtgaggagacagagttaaactggt 594  
DB 301 ACTCCTTATTTATCCAGGGTTGTAGAGATTTGAGATGGAGACGGGAGTCAAACTCAAT 360

QY 595 ccagttatgtcagatagctcaaaatattcgtgtgacaaaggaagcattgggaagtgcc 654  
DB 361 CCAGTTCTGTGAAAGCTCAAAAGTATACCAGATCACCATAGAACCCCTGGAGCTGCT 420

QY 655 tatgagaaagcaagagaggaataacatcagagtaaaaggtttactgatccaaatccatca 714  
DB 421 TATGAACCCGACAAAGAGTGCATCAAGGTAAAGGGTTTGTGTATTAACCAACCCATCA 480

QY 715 aatccattagggcaaatcaggacagaaacacacgtgagaaacgtggtgagcttcaaat 774  
DB 481 AACCCACTGGGAACAATTTATCAAGGACACATTAGAAGCTCTAGTCACTTCAACCAAC 540

QY 775 gagaagcgtatccacctgtatgtatgataatatatgct-gcaacagtttccagccaa-- 831  
DB 541 CACAAGAACATTCATCTGGTGTGTGATGAGATATATGCTGTTACCGTCTTCAGCCGAG 600

QY 832 cccgggttcaatagcatagctagatattagaggtgaaacagacatagagtgaccgc 891  
DB 601 GCCGAATTCACGACATAGCCGAGATAATTTGAAGAAGATA---AAATTTGTTGCAATCGT 657

QY 892 aactcgtcacacattgtttatagcttccaaagacatgggttccctgcttcagagtc 951  
DB 658 GATCTCATCCACATCATTTACAGTTTATCCAAAGACATGGGATTCCTGGATTTAGAGTT 717

QY 952 ggcataatactcttacaatgatcgtgtgtgttaattgtgcacgcaaaatgtcaagcttt 1011  
DB 718 GGCATTGTGTATTATACATAATGATGACGTGGTGTGAGTTGCTCGTAAGATGTCGAGCTTC 777

QY 1012 ggattgggtcaacacagactcagatctcttttagcatcgtatgctaaatgatgatgattt 1071  
DB 778 GGCTAGTATCTTCGAAACCCAGTATCTGATTGCTATGATGCTGATGATGATGATGATGAT 837

QY 1072 gtggagaggtttctgcagagagtgcaagaggttggctcaaggttcagggttttcaact 1131  
DB 838 GTAGACAAATTTATTTGATGAGACGAAAGAGGCTGGCAATGAGACATAGTTTTTTCACA 897

QY 1132 ggggggttggccaaagtgtgcataaaagtctgtcgaagcaaatgctgctctatttgtgtg 1191  
DB 898 CAAAGACTTGTCAAGTAGGCATTAAGTGTGTTTAAAGCAATGCTGCTGCTTTTGTGTGG 957

QY 1192 atgatttaaggcaactctcaaaaaaaccaactctcactctgtgaaacggagctttggaaa 1251  
DB 958 ATGATTGTCGTAGACTGCTGAAAGAACACAGACATTTGAAGCAGAAATGCTGTTATGGAGA 1017

QY 1252 gttatcatcattgaagtttaagatcaatgtttccactgagctattctccattgcactgag 1311  
DB 1018 GTAATTATAACGAAATGAAGAACTCAATGATATCTCTGTTGCTGCTTTCCACTGCTCAGAA 1077

QY 1312 ccagggtggttttaggggtgctgctatgc 1337  
DB 1078 CCGTGGCTGGTTCAGCGCTGCTGCTTGC 1103

RESULT 15  
US-09-043-627-7  
; Sequence 7, Application US/09043627  
; Patent No. 6124525  
; GENERAL INFORMATION:  
; APPLICANT: Botella, Jose Ramon  
; TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.  
; STREET: 100 Thanet Circle, Suite 306  
; CITY: Princeton  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08540-3662  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/043,627  
; FILING DATE: 20-MAR-1998  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU96/00591  
; FILING DATE: 20-SEP-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PMS559  
; FILING DATE: 20-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PMS603  
; FILING DATE: 02-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bernstein, Scott N.  
; REGISTRATION NUMBER: 38,827  
; REFERENCE/DOCKET NUMBER: 3573-1105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-924-8555  
; TELEFAX: 609-924-3036  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1096 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1095  
US-09-043-627-7

Query Match 29.5%; Score 567.8; DB 3; Length 1096;  
Best Local Similarity 70.4%; Pred. No. 1.3e-163;  
Matches 777; Conservative 0; Mismatches 317; Indels 9; Gaps 1;

QY 235 caaatgggttctgtgagatcagcttaccctctgatttggttaagattgatactgaac 294  
DB 1 CAGATGGCCCTTGTGCGAAGATCAGCTTTGCTTTGATTGATCGAAGACTGGATTTCGCAA 60



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 22:51:49 ; Search time 3456.34 Seconds  
(without alignments)  
7509.286 Million cell updates/sec

Title: US-09-763-957-1  
Perfect score: 1923  
Sequence: 1 atcctctccacttactt.....aggcttcaattcattcc 1923

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST:\*
- 1: em\_estba:\*
  - 2: em\_esthum:\*
  - 3: em\_estin:\*
  - 4: em\_estmu:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_hic:\*
  - 9: gb\_esti:\*
  - 10: gb\_est2:\*
  - 11: gb\_hic:\*
  - 12: gb\_gss:\*
  - 13: em\_gss\_hum:\*
  - 14: em\_gss\_inv:\*
  - 15: em\_gss\_pin:\*
  - 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	450.4	23.4	536	9	AW458572	AW458572 sh10h02.y
4	396.2	20.6	651	10	BF649567	BF649567 NF079G12E
5	388.6	20.2	507	10	BI974504	BI974504 sal169d09
6	356.8	18.6	775	10	BM412805	BM412805 EST587132
7	351.8	18.3	623	9	AW560294	AW560294 EST315342
8	349	18.1	479	10	BM095045	BM095045 saj25f06
9	344	17.9	630	10	BF650933	BF650933 NF102806E
10	336.2	17.5	766	10	BM410886	BM410886 EST585213
11	334.8	17.4	653	10	BF648314	BF648314 NF046D07E
12	323.4	16.8	672	9	AI898099	AI898099 EST267542
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14	321.2	16.7	575	9	AI484859	AI484859 EST243120
15	316.2	16.4	819	10	BI421967	BI421967 EST532633
16	314	16.3	573	9	AI165890	AI165890 B003P14U
17	311	16.2	704	10	BI921823	BI921823 EST541726

18	290.6	15.1	428	9	AV410488	AV410488 AVA10488
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21	281.6	14.6	658	9	AI487009	AI487009 EST245331
22	280.8	14.6	644	9	AI727528	AI727528 BNIGH1833
23	280.2	14.6	373	9	AW102376	AW102376 sg86h10.y
c 24	279.8	14.6	517	10	BI921101	BI921101 EST541004
25	276	14.4	628	9	AI727478	AI727478 BNIGH1805
26	272.8	14.2	548	9	AI485016	AI485016 EST243296
27	271.4	14.1	361	9	AW781512	AW781512 sl79h01.y
28	270.6	14.1	503	9	AI490629	AI490629 EST249183
29	269.6	14.0	618	10	BM110122	BM110122 EST557658
30	267.8	13.9	636	9	AI485332	AI485332 EST243653
31	267.6	13.9	595	9	AI897818	AI897818 EST267261
32	265.4	13.8	632	9	AI485399	AI485399 EST243720
33	265	13.8	831	10	BF272588	BF272588 GA_EB001
34	264	13.7	637	9	AW441375	AW441375 EST310771
35	259.8	13.5	585	9	AW618679	AW618679 EST320665
36	257.8	13.4	429	9	AV407744	AV407744 AVA07744
37	251.6	13.1	564	9	AI490418	AI490418 EST248744
38	251.6	13.1	605	9	AI485635	AI485635 EST243956
39	247.4	12.9	513	9	AI487898	AI487898 EST246220
40	247.2	12.9	466	9	AI899645	AI899645 EST269088
41	247.2	12.9	583	9	AI731106	AI731106 BNIGH1871
42	241.8	12.6	721	10	BG645853	BG645853 EST507472
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45	237.2	12.3	462	9	AI488097	AI488097 EST246419

ALIGNMENTS

RESULT 1  
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LOCUS GM830011A1G11 Gm-r1083 Glycine max CDNA clone Gm-r1083-4149 3',  
DEFINITION mRNA sequence.  
ACCSSION BI970666.1 GI:16345071  
VERSION BI970666  
KEYWORDS EST.  
SOURCE soybean.  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 799)  
AUTHORS Vodka L., Keim P., Shoemaker R., Retzel E., Khanna A., Corryell V., Expelid J., Raph C., Shoop E., Pardini J., Liu L. and Lewin H.  
TITLE A Functional Genomics Program for Soybean (NSF 9872565)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: BE020529 corresponding to Gm-cl028-6796 (5')  
Contact: Vodka L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)  
Lewin, H. A., Director, Keck Center for Comparative and Functional Genomics  
University of Illinois  
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA  
Tel: (217) 244-6147  
Fax: (217) 333-4582  
Email: l-vodka@uiuc.edu  
This clone is available through: Incyte Genomics, 4633 World Parkway Circle St. Louis, Missouri 63134. Phone (800) 430-0030 or (314) 427-3222 FAX: (314) 427-3324. Web site: <http://www.incyte.com/reagents/catalog.jsp?page=clones/collaboratio n/index>  
Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.

FEATURES  
source location/Qualifiers  
1..799  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="Gm-r1083-4149"

/clone\_lib="Gm-r1083"

/note="The library Gm-r1083 is a sequence-driven, rereacked set of 4,992 clones selected from cDNA libraries from various tissues and stages of development of soybean. It represents 1117 sequences from the progenitor library Gm-cl009 (from mature roots of 2 month old greenhouse grown 'Williams' soybean plants); 820 sequences from the progenitor library Gm-cl013 (from 2 to 3 week old whole plants of Williams); and 3055 sequences from library Gm-cl028 (from 'Supernod' plants whose seedlings were inoculated with Bradyrhizobium japonicum, courtesy of Dr. Gary Stacey). The 5' ESTs of the source clones from the different progenitor libraries was used to select singletons, or a representative of each contig, which were rereacked to form library Gm-r1083. The cDNA clones of the rereacked Gm-r1083 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, <http://web.ahc.umn.edu/biodata/nsfsyf/>. Rereacking was performed by Incyte Genomics, St. Louis, <http://www.incyte.com>, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, <http://www.lie.uiluc.edu/biotech/keck.html>. Note: The corresponding 5' EST from each clone in the Gm-r1083 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Incyte Genomics clone ID of the original cDNA library that is also listed under 'OTHER EST'."

BASE COUNT 256 a 168 c 139 g 215 t 21 others  
ORIGIN

Query Match 25.8%; Score 496.6; DB 10; Length 799;  
Best Local Similarity 81.3%; Pred. No. 3.3e-113;  
Matches 642; Conservative 0; Mismatches 125; Indels 23; Gaps 6;

QY 1149 tggcataaagtcgttgcaagcaatgctgtctattgtgtgtaggttaaggcaact 1208  
|||||  
DB 799 TGGCATAAAGTGC-TGCAANNATGCTGTGCTCTTTGTGTGATGATNNAGGCAACT 741  
QY 1209 tctcaaaaagcaactttcagactgaaacggagctgtttggaaagtatactcaatgaagt 1268  
|||||  
DB 740 NNTCAAGAAGCCACGCTTGACTCTGAAATNNNGCTTTNNAGAGTGATCATTTGATGAGGN 681  
QY 1269 taagatcaatgtttcactcggctattccctcattgctgactgagccagggtgtttagggt 1328  
|||||  
DB 680 NAAGATCATGTTTACCTGGCTCCTCTCTTCCATTGCACTGAGCCAGGGTGTNNNGGT 621  
QY 1329 gtgctatgccaacatggtatgctgtgtgcaaatgtgcttgcacacgaatccgcaactt 1388  
|||||  
DB 620 GTGCTATGCCAACATGGATGATGCTGTGCAAAATTCGATTTGCAAGAATTCGTAACTT 561  
QY 1389 tttgtcttcaaaaagagggtggtgtgtcttaataagaacaatttggcacagtaactt 1448  
|||||  
DB 560 TGTGCTTCAAAAACAGGAGATCATGGTGCCTAACAAAGAAACAAATTGTTGCCACAGTAAC 501  
QY 1449 gaggctgagcctcaaaacaggaaggtttgatgatcatcaccatgtcacctcactctcccc 1508  
|||||  
DB 500 GAGGTGAGCCCTCAAAACAGGAGGTGTTGATGATCATGATGATGATGATGATGATGAT 441  
QY 1509 acctcagtcacactatggtttaaaggccacaaattgagtttgcatattcctcctgaatgttta 1568  
|||||  
DB 440 ACCTCAGTCACCTCTGGTTTAAAGCCACAAATTTGAGTTGGCATATTTCTGTAACCCCTCTA 381  
QY 1569 gaagaagtaactgatgatggaagattacttgggtttctttttattttttattttttgagaggtta 1628  
|||||  
DB 380 GAAGAAGTAACATGATATGATGATGATATTTGTTGGCTCTTTTGACATGTTGTTTGGCAGGTA 321  
QY 1629 cataa--gtgctggattgtttctttggaacagcagaataacaggaattctctgtgtgttt 1686  
|||||  
DB 320 CATAAAGTCCTGAGTTGTTGTTATTTTAAACACAGCATACAGGCATGCTGTATATGTTT 261

QY 1687 tgtgatc-----ggcatcacatccagtgctcctcaaatgtgtgctgcttcatgcac 1737  
|||||  
DB 260 TTGTTTACCACATCCAAAGTCTCTTTGCCTTGGTGCATAGAACTTGTGCTACTGGAACAT 201  
QY 1738 gcccttcaactttagggg-----catttttcttttttccacttaccaaa-----ggttc 1787  
|||||  
DB 200 GCCCCTTCAATTTTAGGGGCAATTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 141  
QY 1788 aagggtgaaaaagtattatagatgctgtaattgtattgttttgcataagaagagcccaaaaga 1847  
|||||  
DB 140 AAGGTGAAAAAGTTTATAGAGTTTGTAAAGGTTATTTGGTTTATTAGAGAGTCCGAAGA 81  
QY 1848 tctctgtaattctgactgactgaaattgttaactttcaatttgaataataatttataaagt 1907  
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DB 80 ACTCTGTATTCTTATACGTCATTTGTA--GCTCGATGATCAATAAATTTGTTAATAGAGG 22  
QY 1908 ctccaattc 1917  
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DB 21 NNTCAATAC 12

RESULT 2  
BE020529 578 bp mRNA linear EST 03-DEC-2001  
LOCUS sm44h02.y1 Gm-cl028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
DEFINITION Gm-cl028-6796 5' similar to SW:IAIC.SOYBN P31531  
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ; mRNA sequence.  
ACCESSION BE020529  
VERSION BE020529.1 GI:8282968  
KEYWORDS EST.  
SOURCE soybean.  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
REFERENCE 1 (bases 1 to 578)  
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna  
A., Bolle,B., Warra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished (1999)  
CONTACT: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Hunttsville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: ccu@resgen.com  
Insert Length: 3902 Std Error: 0.00  
High quality sequence stop: 390.  
FEATURES  
Location/Qualifiers  
1..578  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-6796"  
/clone\_lib="Gm-cl028"  
/tissue\_type="roots of 'Supernod' plants"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II XR; Site\_1: EcoRI; Site\_2:  
XhoI; The mRNA was isolated from roots of Glycine max  
'Supernod' plants generously donated by Dr. Gary Stacey.  
The seedlings were inoculated with Bradyrhizobium  
japonicus, strain USDA110 prior to harvest. StrataGene's  
cDNA synthesis Kit (catalog number 200401) was used to  
synthesize the cDNA. First-strand synthesis was performed

with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A-C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAACTAGTCTCGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell.

BASE COUNT 178 a 115 c 136 g 149 t  
ORIGIN

Query Match 25.3%; Score 486.8; DB 9; Length 578;  
Best Local Similarity 90.1%; Pred. No. 8.5e-111;  
Matches 521; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 236 aaatggcttctgtgagaatcagctaccctgtgattggtgaagattgatactgaaca 295  
|||||  
Db 1 AAATGGGCTTTCGTGGAATCAGCTTACTTCTGATTGGTGAAGATGGATCTGAATA 60  
QY 296 accctgaagctctcattgctactcagaagaataaaatgatttcaggggccatagctaact 355  
|||||  
Db 61 ACCCAGAGCGCTCCATTTCACACACAGAGGAATAAATGATTTCAGCGCCATAGCTAACT 120  
QY 356 ttcaggattatcatggtctgcccagagtcagaaaatgctgtgctaaatttatggctagaa 415  
|||||  
Db 121 TTCAGGATTATCATPCTGCTGCCGAGTTCAGAAATGCTGTGGCTAAATTCATGGGTAGAA 180  
QY 416 caagggaaacagatcacgtttgacctgacccgtatgctatgctagcggtgagccaccg 475  
|||||  
Db 181 CAAGAGAAACAGAGTACGCTTTCCTGACCGTATGTGATGAGCGGTGGAGCAACTG 240  
QY 476 gagcacacgaagtcactgccttttggcagatcccgccgagcgcatctcttagtgcaca 535  
|||||  
Db 241 GAGCACACGAAGTCACTACCTTTTGTGGCAGACCCCTGGTGACGCATTTTGTGTGCCCA 300  
QY 536 ttcctattatccaggctttgacgggatttgaggtgagagaacaggaggttaaacctgttc 595  
|||||  
Db 301 TTCCTTATTATCCAGGTTTGGACGGGATTGAGGTGGAGAACAGGAATTAACCTTGTTC 360  
QY 596 cagtattgtcgatagctcaataattcgtgttgacaagaagcattggaagatccct 655  
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Db 361 CAGTTATGTGGATAGTCTCAACAAATTCAGTTGACAAGCAAGCAATTTGGAAGATCGGT 420  
QY 656 atgagaagcaagagagagataaatactcagatgataaggggtttactgatccaccaatccatcaa 715  
|||||  
Db 421 ATGAGAAGGCCAAAGAGGATAATATAAGATTAAGAGGCGCTTGCTCATCACCACCAATCCATCAA 480  
QY 716 atccattaggacacaatcatgagagaagaacactgagaacccgtggtgagcttcatcaatg 775  
|||||  
Db 481 ACCATTAGGCACAGTCTATGACAGAAACACACTAAGAACCCTGATGAGCTTCATCAACG 540  
QY 776 agaagcgtatccacctgtgtgatgataaataatgct 813  
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Db 541 AGAAGCGTATCCACCTTGATCTGATGAATATATCTCT 578

RESULT 3  
AW458572

LOCUS  
DEFINITION  
AW458572 536 bp mRNA linear EST 03-DEC-2001  
sh10h02.y1 Gm-cl016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
Gm-cl016-4396 5' similar to SW:IA1C.SOVBN P31531  
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ; mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AW458572.1 GI:7028789  
EST.  
soybean.  
soybean.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
REFERENCE  
1 (bases 1 to 536)  
Shoemaker, R., Keim, P., Vodkin, L., Erpeliding, J., Coryell, V., Khanna  
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers  
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk  
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann  
R., Witterson, R. and Wilson, R.  
Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 for further information  
call: (800)-533-4363 or contact via email: ccu@resgen.com  
Insert Length: 1062 Std Error: 0.00  
Seq primer: -40RP from Gibco  
High quality sequence stop: 427.  
FEATURES  
source  
Location/Qualifiers  
1..536  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl016-4396"  
/clone\_lib="Gm-cl016"  
/tissue\_type="immature flowers of field grown plants"  
/lab\_host="Xl10-Gold"  
/note="Vector: pBluescript II XR; Site\_1: EcoRI; Site\_2:  
XhoI; This cDNA library was constructed from mRNA isolated  
from immature flowers of field grown plants. The cDNA  
library was prepared using the Stratagene pBluescript II  
XR library construction kit. Complementary DNA was  
synthesized from mRNA using a primer consisting of a poly  
(dT) sequence with a XhoI restriction site. EcoRI adapters  
were ligated to the blunt-ended cDNA fragments followed by  
XhoI digestion. The cDNA fragments were directionally  
cloned into the EcoRI-XhoI restriction site of the  
pBluescript vector. The ligated cDNA fragments were  
transformed into XL10-Gold host cells. This library was  
constructed by Dr. Randy Shoemaker and Dr. John  
Erpeliding."  
BASE COUNT 147 a 105 c 134 g 149 t 1 others  
ORIGIN  
Query Match 23.4%; Score 450.4; DB 9; Length 536;  
Best Local Similarity 91.0%; Pred. No. 1e-101;  
Matches 478; Conservative 0; Mismatches 47; Indels 0; Gaps 0;  
QY 1005 aagctttggattggtgtcaacacagactcagatctcttttagcatcgatgctaaatgatga 1064  
|||||  
Db 8 AAGCTTTGGGTTGGTGTCAACACAGACAGCTAGCATCTCTTTAGCAATCAATGCTAAATGATGA 67  
QY 1065 tgagttgtgagagaggtttctgagagagtgcaaaaggtgttgctcaaggttcagggt 1124  
|||||  
Db 68 TGAGTTTGTGGAAGGTTTCTGGGAGAGAGTGCAAAAAGGTTTGGCACAAGGCATAGAGT 127

QY 1125 ttctactggggggttgcccaagttggcataaagtcgttgcaaaagcaaatgctggtctatt 1184  
|||||  
Db 128 TTTCACTTCGGGGTTGGCCAAAGTTGGCAATAAGTCTTGCAAGCAATGCTGGTCTCTT 187  
  
QY 1185 tctgtgagtgatttaaggcaactctcaaaagccaactttcgcactctgaacagagct 1244  
|||||  
Db 188 TGTGTGATGGATTTAAGCAACTTCTCAAGAAGCCACAGCTTGACTCTGAATGGAGCT 247  
  
QY 1245 ttgaaaaattcatcatgaagttaagatcaatgtttcacctggctattcccttcattg 1304  
|||||  
Db 248 TTGGAGAGTGATCAATCATGAGGTTAAGATCAATGTTTCACCTGGCTCTCTTCCATTG 307  
  
QY 1305 cactgagccaggggttggttaggggtgctatgccaaactggatgatgctggtgcaaat 1364  
|||||  
Db 308 CACTGAGCCAGGGTGTGTAGGGTGTGATGCCAACATGGATGATATGGCTGTGCAAA 367  
  
QY 1365 tgccttgaacaaatccgcaacttctgcttcaaaacagagggtcggtgtctaaataa 1424  
|||||  
Db 368 TGCATTGCCAAAGATTCGAACCTTCGTCTTCAAAACAGGAGGTCATGGTTCCTAACA 427  
  
QY 1425 gaaacattgttggcagtaacttgaggtgagctcctcaaaacagaggttttgatgat 1484  
|||||  
Db 428 GAAACATTGCTGSCACAGTAATCTGAGGTTGAGCCTCANNACCAGAGGTTTGATGAT 487  
  
QY 1485 caccatgtcaactcactccctccactcactcagtcacactatggttaa 1529  
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Db 488 CATGATGTCACTCACTCCCTATATACCTCAGTCCGCTTGGTTAAA 532

RESULT 4

BF649567 LOCUS BF649567 651 bp mRNA linear EST 20-DEC-2000  
DEFINITION NF079G12EC1F1099 Elicited cell culture Medicago truncatula cDNA  
clone NF079G12EC 5', mRNA sequence.

ACCESSION BF649567  
VERSION BF649567.1 GI:11914697

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM

Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 651)  
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation -  
Center for Medicago Genomics Research

JOURNAL Unpublished (2000)

COMMENT Contact: Dixon RA  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7302  
Fax: 580 221 7380

Email: radixon@noble.org  
Insert Length: 651 Std Error: 0.00  
Plate: 079 row: G column: 12

Seq primer: TCACACAGGAACAGCTATGAC.  
Location/Qualifiers  
1, 651  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="NF079G12EC"

/clone\_lib="Elicited cell culture"  
/tissue\_type="Cell suspensions derived from root tissues"  
/dev\_stages="Cell suspensions were subcultured every 14  
days. Cells were induced six days after subculture"

/note="Vector: Lambda Zap; Cells were induced with yeast  
cell wall extracts equivalent to 50ug/ml glucose in the  
final concentration. Samples were taken at 0.5, 1, 12 and  
24 hours after induction. Equal amounts of RNA from each  
time point were pooled and used for mRNA isolation."

FEATURES

SOURCE

BASE COUNT 207 a 83 c 147 g 210 t 4 others  
ORIGIN  
  
Query Match 20.6%; Score 396.2; DB 10; Length 651;  
Best Local Similarity 77.7%; Pred. No. 3.7e-88;  
Matches 505; Conservative 0; Mismatches 136; Indels 9; Gaps 2;  
  
QY 853 gagatattagaggtgaacacagacatagagtgcacgcgaacctcgttacacattggttat 912  
|||||  
Db 1 GAATATATTAGACATGACACACACATTAATGTGACCGTAACTCGTTCAACATAGTTTAC 60  
  
QY 913 agtctttcaaaaggatgggttccctggcttcagagtcggcatcatatactcttacaat 972  
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Db 61 AGTCTTTCAAAAGACATGGGATTCCTGGTTTAGAGTTGGTATAATATACTCTTATAAT 120  
  
QY 973 gatgtgtggttaattgtgcacgcaaaatgtcaagctttgggattgggtgtcaacacagact 1032  
|||||  
Db 121 GATACCGTTGTAATTTGTGCACGAAATAATGTCAAGTTTGGATTTAGTTTCAACACACAGACA 180  
  
QY 1033 cagtatcttttaagcatcgatgctaaatgatgatgttctgtgagaggtttctctggcgagag 1092  
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Db 181 CAATACTTGATGCCGAAATGCTGCTGATGACGAGTTCGTTAAAAAGTTTCTTACTGAA 240  
  
QY 1093 agtgcacaagaggttggtgcataaagggttcaggggttttcaactgggggtggccaaagtgtgc 1152  
|||||  
Db 241 AGTGCAAAAGAGGTTAGCACAAAGGTACAGAAATTTTCCACGATGGATTAAACCAAGTTGA 300  
  
QY 1153 ataaagtcttgcacaagaatcgtgctctattgtgtgagatgatttaagcaactcttc 1212  
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Db 301 ATTAATTTGTTTACAAGTAACCGTGGACATTTTGTGTGGATGGATTTGAGAGGACTTCTT 360  
  
QY 1213 aaaaagccaaactttgcactcttgaacggagctttgaaagtattcattcatgaagttaag 1272  
|||||  
Db 361 AAGGAAGCTACATTTGAATCAGAAATTTGGAACATATGAGAGATGATTTATCCACGAAGTTAAG 420  
  
QY 1273 atcaatgtttccacctggctattcctccatctgcactgagccgggtggttgggtgtgctg 1332  
|||||  
Db 421 ATTAATGTTTCACTGGTGTCTTTTTCATTGTTTGTGAGCCAGGGTGGTGTAGTGTGT 480  
  
QY 1333 tatgccaacatgatgatgctgtgcaaatgtcttgcacaacgaatccgcaactttgtg 1392  
|||||  
Db 481 FATGCTAACATCGATGATAGACATGTGCCAAATTTGCTTTTACAAGGATTAAGTTCATTGTG 540  
  
QY 1393 cttc---aaaaaaggagtcgtggtgtctaataag-----aacattgttggcacat 1443  
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Db 541 GTTCAGAAATAAAGAGAGTTATGTTGCTGTGANAANAACACTAAACCTTGTGGCATACT 600  
  
QY 1444 aacttgaggtgagcctcaaaaccagagaaggtttgatgatcaccatgtc 1493  
|||||  
Db 601 AATTTGAGGTTAAGCCTTAAAAACAAGANGTTTGATGATATTATGTATGTC 650

RESULT 5

BI974504 LOCUS BI974504 507 bp mRNA linear EST 30-NOV-2001  
DEFINITION sai69d09.y1 Gm-cl068 Glycine max cDNA clone GENOME SYSTEMS CLONE  
ID: Gm-cl068-4001 5', similar to SW:1A1C.SOVBN P31531  
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;, mRNA sequence.

ACCESSION BI974504

VERSION BI974504.1 GI:16348909

KEYWORDS EST.

SOURCE soybean.

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phascoleae;  
Glycine.  
1 (bases 1 to 507)

REFERENCE

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna  
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk





Db 121 AGAAGCATATGAAATGCACAAAAATCAAAACATCAAAAGTAAAGGTTTGATTTTGACCAA 180

Qy 708 tccatcaaatccattaggcacaacatcatggacagaaagacactgagaacccgtgtgagctt 767

Db 181 TCCATCAATCATTTGGGACCACATTTGGACAAACACACACTGAAAGTGCTTTGAGTTT 240

Qy 768 catcaatgagaagcgtatccaccttgtatgtgatgaatatatgtgtgcaacagttttcag 827

Db 241 CACCAACCAACAACATCCACCTTGTGTGACGAAATCTACGCAACGACACTGCTTTGA 300

Qy 828 caaacccgggttcataagcatagctgagatatagaggatgaaacagacatagatgtga 887

Db 301 CAGGCTCAATTCGTCAGTATAGCTGAATCCCTCGATCAACAGSAAATCACTTACTGCAA 360

Qy 888 ccgcacccctcgacacattgtttatagctcttcacaaagacatgggggttccctggctcag 947

Db 361 CAAGATTGATTCACATCGCTACAGCTCTTCAAAAGACATGGGGTTACAGAGATTAG 420

Qy 948 agtcggcatcatatactcttaacatgatgctgtgtgttaattgtgacgcacaaatctcaag 1007

Db 421 AGTCGGAATCATATATTTCTTTTAAAGCAGCATGCTGTTAATTGTCTAGAAAAATGTCGAG 480

Qy 1008 ctttgattggtgcaacacagactcagtatcttttttagcatcgatgctctaaatgatga 1067

Db 481 TTTTCGGTTAGTATCTACACAAACCAATATTTTTTAGCGCAATGCTATCGGACGAAAA 540

Qy 1068 gtttggagaggtttcttggcagagtgcaaaagaggttggctcaaaagtttcagggtttt 1127

Db 541 ATTCTCGATATTTTCTTAAGAGAAAGCGGATGAGTTAGTAAAGGCAAAACATTT 600

Qy 1128 cactgggggggttggcacaagttggcatataaagtctgtgcaaaagcaatgctgtctattgt 1187

Db 601 TACTAATGGACTTGAAGTAGTGGGAATTAATGCTTGAATAATAATGCGGGCTTTTGTG 660

Qy 1188 gggatgatttaaggcaactctcaaaagccaaactttcga-ctctgaaacggagcctt 1246

Db 661 TTGGATGATTTTCGTCACATTTTAAAGGAATCGACTTTCGATAAGCGAATGTCGCTTAT 720

Qy 1247 ggaaggttatcatcatgaagtaagatcaatgtttccacctggctattcctt 1298

Db 721 GGAGAAGTATTATAACGATGTTAAGCTTAAGCTCGCTCGCTTGGATCTTCGTT 772

RESULT 7

AW560294/c

LOCUS

DEFINITION

623 bp mRNA linear EST 07-SEP-2000

EST315342 DSIR Medicago truncatula cDNA clone pDSIR-26N23, mRNA

ACCESSION

AW560294

VERSION

AW560294.1

GI:7205720

KEYWORDS

EST.

SOURCE

barrel medic.

ORGANISM

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE

1 (bases 1 to 623)

Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.

ESTs from roots of Medicago truncatula after inoculation with Phytophthora medicaginis

UNPUBLISHED (1999)

Contact: Carroll P. Vance

Department of Agronomy and Plant Genetics

University of Minnesota

411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA

Tel: 612 625 5715

Fax: 651-649-5058

Email: vance004@maroon.tc.umn.edu

Minnesota EST name:M251649e ; TIGR sequence name:MTBAW84TK ; More information, including clone ordering, is available at. .

FEATURES

source

'http://chryslie.tamu.edu/medicago'

Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

Location/Qualifiers

1..623

/organism="Medicago truncatula"

/cultivar="genotype Al7"

/db\_xref="taxon:3880"

/clone="pDSIR-26N23"

/clone.lib="DSIR"

/tisue\_type="roots infected with Phytophthora medicaginis"

/dev\_stage="roots harvested at 10 days post inoculation with Phytophthora medicaginis"

/lab\_host="E. coli strain XL0LR"

/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10 days post inoculation with Phytophthora medicaginis. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XL0LR cells. Note: EST may be of fungal origin."

BASE COUNT 205 a 138 c 83 g 197 t

ORIGIN

Query Match 18.3%; Score 351.8; DB 9; Length 623;

Best Local Similarity 77.1%; Pred. No. 4.5e-77;

Matches 457; Conservative 0; Mismatches 127; Indels 9; Gaps 2;

Qy 962 actcttacaatgatgctgtggttaattgtgcacgcgcaaaatgcgaagcttggattggtgt 1021

Db 623 ACTCTATAATGATACCGGTGTAATTTGTCGACGAAATGTCAGTTTGGATTAGTTT 564

Qy 1022 caacacagactcagtatcttttagcatcgatgctaagtatgatgattgttgagaggt 1081

Db 563 CAACACAGACACAATACTTGTATGGCGCAAAATGCTGCTGATGACGAGTTCGTTAAAAAGT 504

Qy 1082 ttctggcagagagtcaaaaggttggctcaaaagttcagggttttccactgggggttgg 1141

Db 503 TTTTACTGAAAGTCAAAGAGGTTAGCACAAAGGTACAGAAATTTTCACAGTGGATTAA 444

Qy 1142 ccaagttggcataaagtgtctgcaaaagcaatgctggtctattgtgtggatggatttaa 1201

Db 443 CCAAGTTGGAATTAATTTGTTACAAAGTACGGTGGACTTTTGTGTGGATTGCA 384

Qy 1202 ggcacacttcacaaagccaaactttcgcactctgaaacggagctttggaaagtatcatc 1261

Db 383 GAGGACTTTTAAAGGAAGCTACATTTGMAATCAGAAATTTGGAACCTTGGAGAGTATTTC 324

Qy 1262 atgaagttaaagatcaatgtttcacctggctattctcctcactgacactgacccaggtgt 1321

Db 323 ACCAAGTTAAGATTAAATGTTTCCACCTGGTGTTCCTTTTCATTGTTCTGAGCCAGGGTGT 264

Qy 1322 tttaggtgtgctatgccacatggatgatgctgtgcgaattgtttgcaacgaatcc 1381

Db 263 TTAGAGTGTGTTATGCTACATGATGATAGAGATGTGCATAATTCGTTTACAAAGGATTA 204

Qy 1382 gcaactttgtgcttc---aaaacaaggaggtcgtgtgctcctaataag-----aaacatt 1432

Db 203 GGTCAATTTGTGTTGAGAAATTAAGGAGGTTATGTTGCTCTGAGAAACACATAAACCTT 144

Qy 1433 gttgcacagtaacttgaggctgagccctcaaaacagaaggtttgatgatcatcaccatgt 1492

Db 143 GTTGGCATAGTAATTTGAGCTTAAGCCTTAAACAAGAAGGTTTGATGATATTGTAATGT 84

Qy 1493 caccctactctcccctacccctcagtcacctatggtttaaaagccacaataatgagtt 1545

Db 83 CACCTCATTTCTCCATTTCTCCTCAGTCACCTCTTGTGTTAAAGCCACTACTTGAATT 31

Db	61	CTGAGCAGCGTGGTTTGGGTTGCTATGTCACCATGATGATGCTGTGCAAAATTG	120
QY	1367	ctttgcaacgaatccccaacttggcttcaaaaacgaagaggtcgctgctctaataaga	1426
Db	121	CATTGCAAGAATTCGTAACCTTGTCTTCAAAACAGAGGATCATGGTCCCTACACA	180
QY	1427	aacattgttgccacagtaacttgaggctgagcctcaaacacgaagggtttgatgatca	1486
Db	181	AACATTGTTGGCACAGTAACCTTGAGGTGAGCCTCAAAACCAAGAGTTTGATTATCA	240
QY	1487	ccatgcaactcaactccctccactccctcagtcacccatggttaaaacacaaatgagttt	1546
Db	241	TGATGTACCTCACTCCCCATACCTCAGTCACCTTGGTTAAAGCCACAATTTGAGTTG	300
QY	1547	gcattctctgaactgtttagaagaagtaactgatgtgaagattacttggttcttt	1606
Db	301	GCATATTCTCTGAACCTCTAGAGAAGTAAGTATATGATGATTATTTGGTCTCTTT	360
QY	1607	tattgttattttgagaaggtacataa--gtcgtgatttcttcttgaacagcaataa	1664
Db	361	GACTTGTGTTTGGCAAGGTACATAAAGTGGCTTGAGTTTGTATTATTTAACAGCAGTAA	420
QY	1665	caggaattctcgtatgtttttt	1687
Db	421	CAGGCAATGCTGATATGTTTT	443
RESULT	9		
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LOCUS			
DEFINITION		630 bp mRNA linear EST 20-DEC-2000	
ACCESSION		clone NF102B06EC 5', mRNA sequence.	
VERSION		BF650933	
KEYWORDS		EST.	
SOURCE		barrel medic.	
ORGANISM		Medicago truncatula	
REFERENCE			
AUTHORS		Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.	
TITLE		Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research	
JOURNAL		Unpublished (2000)	
COMMENT		Contact: Dixon RA Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7302 Fax: 580 221 7380 Email: radixon@noble.org Insert length: 630 Std Error: 0.00 Plate: 102 row: B column: 06 Seq primer: TCACACAGGAACACGCTATGAC.	
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		/clone="NF102B06EC"	
		/tissue_lib="Elicited cell culture"	
		/tissue_type="Cell cultures derived from root tissues"	
		/dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"	
		/note="Vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."	
		186 a 115 c 121 g 205 t 3 others	
BASE COUNT			
ORIGIN			

Query Match	17.9%;	Score 344;	DB 10;	Length 630;	
Best Local Similarity	81.8%;	Pred. No. 4e-75;			
Matches 395;	Conservative 0;	Mismatches 88;	Indels 0;	Gaps 0;	
Qy 88	atgggtttcaaggccatggaccacaaactcccttgtgtccaagatggctatggggatgga	147			
Db 147	ATGGACCTGTGAGCATGGACCAACCTCAATTTGTCTCAAGATAGCCACTGGTGATGGA	206			
Qy 148	catggcgatcatccccactactttgatggatggaagggcttatgatcaaaacccctttcat	207			
Db 207	CATGCTGAACATCATCTTCTTGTGATGATGGAAGCTTATGATTAATAAACCCCTTTTCAT	266			
Qy 208	ccacagataatcctaacggtgttatgcaaatgggtcctgtgagaatcagcttacctct	267			
Db 267	CCAACCAAAAATCCTCAAGGTGTATCCAAATGGGTCTTGCAGAGAAATCAGCTTACTGCT	326			
Qy 268	gatttggttggaagtgtgatactgaacaaacctgaagctccatttgcactccagaagga	327			
Db 327	GATTTGGTTCAAANTTGGATATAGTAACTAACCCAGAAGCTCAATTTGTACTCTAGAAGGA	386			
Qy 328	ataaatgatttcaggcgccatgaacttcaggattatcatggtctggtgagagttcaga	387			
Db 387	GTACACAATTTCAAGAAATGCTTAATTTTCAGGATTTATCTGCTACAGAGTTTACA	446			
Qy 388	aatgctgtgctaaatttatggctagaacaagggggaacagaaatcacgtttgacctgac	447			
Db 447	AATGCTGTGGCTAAATTCATGTCAGAACACAGAGGAAATAGATGACATTTGTACTCTGAT	506			
Qy 448	ctattgtcatgagcgttgagccaccggagcacacaggaagtcactgctttgtttggca	507			
Db 507	CTATTTGTCATGAGTGGGGGCAACTGGAGCATATGAGGCNCGTGCCCTTTGTGTGGCA	566			
Qy 508	gatccggcgagcgattcttagtgcctatccctattatccaggctttgaccggatttg	567			
Db 567	GATCCTGTGTGCTTTTGTGGTGCCTACACCTTACTCCANGATTGATCGAGATTTG	626			
Qy 568	agg 570				
Db 627	ANG 629				
RESULT 10					
BM410886					
LOCUS	EST585213	tomato breaker fruit Lycopersicon esculentum cDNA clone			
DEFINITION	EST585213	tomato breaker fruit Lycopersicon esculentum cDNA clone	linear	EST 22-JAN-2002	
ACCESSION	BM410886				
VERSION	BM410886.1	GI:18262516			
KEYWORDS	EST.				
SOURCE	tomato.				
ORGANISM	Lycopersicon esculentum				
REFERENCE	Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai				
AUTHORS	J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning				
	,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.				
TITLE	Generation of ESTs from tomato fruit tissue, breaker stage (2002)				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: CUGI				
	Clemson University Genomics Institute				
	Clemson University				
	100 Jordan Hall, Clemson, SC 29634, USA				
	Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>				
	This clone is available through the Clemson University Genomics				
	Institute				
FEATURES	Seq primer: T3.				
source	Location/Qualifiers				
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/clone="clEG54P6"  
/clone\_lib="tomato breaker fruit"  
/tissue\_type="pericarp"  
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/lab\_host="SOLR"  
/note="vector: pBluescriptSKMcuadapt; Site\_1: EcoRI;  
Site\_2: XhoI; supplier: Boyce Thompson Institute;  
sequencing: The Institute for Genomic Research. Fruit  
were harvested at the breaker stage (first sign of  
lycopene accumulation on the blossom end of fruit). Fruit  
were cut in half and the seeds and locules were discarded  
prior to freezing the pericarp."  
BASE COUNT 246 a 125 c 150 g 245 t  
ORIGIN

Query Match 17.5%; Score 336.2; DB 10; Length 766;  
Best Local Similarity 69.3%; Pred. No. 3.8e-73;  
Matches 472; Conservative 0; Mismatches 208; Indels 1; Gaps 1;  
Qy 93 ttccaaggccatggaccacaaactcccttgtgtccaagatggctatggggatggacatgg 152  
Db 83 TTCAAAGAAATAACCAAAAAACAACAACTTCTTTCAAAGATAGCTACAAATGATGGTCATGG 142  
Qy 153 cgaatcatccccactactttgatggatggaagcttatgatcaaaacccctttcatccac 212  
Db 143 GGAAAAATTCACCTTATTTGTGATGGTGGNAGGCTTATGCAAAATATCCTTTTCATCTAAC 202  
Qy 213 agataatcctaacggtgttatgcaaatgggtctgtcgtgagaatcagcttacctcgtatt 272  
Db 203 TGATAATCCTACTGCTGTATTTCAGATGGGTCTGGCTGAAATATCAGCTTTGTTTGTATT 262  
Qy 273 ggttgaagatgtgactgaacaaacctgaagcctccatttcactccagagaggaataaa 332  
Db 263 AATCCAAGATGGTGGTGAATAATCCAAAAGCATAATTTGCACCTGTGTAAGAGAGCTGA 322  
Qy 333 tgatttcaggccatagcttaactttcaggattatcatggtctggtcgcgagttcagaatatg 392  
Db 323 AAATTTCCAAGATATTGCAATTTTTCAGATTTATCATGGCTTGCACAGAGTTTAGACAAGC 382  
Qy 393 tgtgctcaaatattatggtctagaaacagggggaaacagaatcagctttgaccctgacctat 452  
Db 383 AGTTGCAAGGTTTATGGAGAAAGTGAGAGGTGACAGAGTTACATTTGATCCAAACAGAAAT 442  
Qy 453 tctcatgagcgttgagccaccggagcacacgaagctcactgctctttgttggcagatcc 512  
Db 443 AGTAATGAGTGGAGGAGCAACTGGTGTCTCATGAATGCTTGTCTTTTGTGCTGATGCC 502  
Qy 513 cggcgaggcattcttagtgcctatccctattatccaggctttgaccgggatttgaggtg 572  
Db 503 TGGTGATGCTTTTGGTCCCAACACCATATTATCCAGGATTTGTAGAGATTTGAGATG 562  
Qy 573 gagaacagaggttaaaactgttccagttatgtgcgatactcaataataattcgtgtgac 632  
Db 563 GAGAACTGGTGTTCAACTATTATTCAGTTCTTTGTTGTAATGATTTCAAAGTGAC 622  
Qy 633 aaagaagcattgggaagctgctatgaaagaagaagagaggaataacatcagagtaaggg 692  
Db 623 TACAAAACGCTTGGGAAGAAGCATATGAAAAGCTCAACATCCACATCAAAATAAAGG 682  
Qy 693 ttctactgacacaaatcccatcaaatccatttaggcacaaatcaggacagagaagacatgag 752  
Db 683 CTTACTTATAAAACAACCCCTTCCAATCCATTAGTAGTACTCTTCTTGACAG-GACACACTCCG 741  
Qy 753 aaccgtggtgagcttcatcaa 773  
Db 742 TGACATTGTGAACGTTTCATCAA 762

RESULT 11

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BF648314      BF648314      .      mRNA      linear      EST 20-DEC-2000
LOCUS        NF046D078C1F1061 Elicited cell culture Medicago truncatula cDNA
DEFINITION   clone NF046D078C 5', mRNA sequence.
ACCESSION    BF648314
VERSION      BF648314.1 GI:11913444
KEYWORDS     EST.
SOURCE       barrel medic.
ORGANISM     Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE    1 (bases 1 to 653)
AUTHORS      Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
              Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
TITLE        Expressed Sequence Tags from the Samuel Roberts Noble Foundation -
              Center for Medicago Genomics Research
JOURNAL      Unpublished (2000)
COMMENT      Contact: Dixon RA
              Plant Biology Division
              The Samuel Roberts Noble Foundation
              2510 Sam Noble Parkway, Ardmore, OK 73402, USA
              Tel: 580 221 7302
              Fax: 580 221 7380
              Email: radixon@noble.org
              Insert Length: 653 Std Error: 0.00
              Plate: 046 row: D column: 07
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                /dev_stage="Cell suspensions were subcultured every 14
                days. Cells were induced six days after subculture"
                /note="Vector: Lambda Zap; Cells were induced with yeast
                cell wall extracts equivalent to 50ug/ml glucose in the
                final concentration. Samples were taken at 0.5, 1, 12 and
                24 hours after induction. Equal amounts of RNA from each
                time point were pooled and used for mRNA isolation."
BASE COUNT   194 a 123 c 118 g 216 t
ORIGIN
Query Match      17.48; Score 334.8; DB 10; Length 653;
Best Local Similarity 82.3%; Pred. No. 8.1e-73;
Matches 395; Conservative 0; Mismatches 84; Indels 1; Gaps 1;

QY  88 atgsgttcaaggccatgaggaccactcccttggtgccaatggcgtattggggatgga 147
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Db  174 ATGGGACTGTGAGCATTGGACCAACCCCAATTTGTTGCCAAGATAGGCATGGTGATGGA 233
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QY  148 catggcgaataatccccatactttgatggatggaggcttatgatcaaaacccctttcat 207
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  234 CATGGTGAACATCATCTTACTTTGATGGATGGAAGCTTATGATAAAACCCCTTTTCAT 293
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QY  208 cccacagataatcctaacggtgttatgcataatgggtttgtctgagaatcagcttacctct 267
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  294 CCAACCAAAAATCTCAAGGTGTTATCCAAATGGGTCTTGCAGAGAAATCAGCTTACTGCT 353
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  268 gatttggtgaagattggactactgaacaacctgaacccctcatttgcactcccagaagga 327
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  354 GATTTGGTTCAAAATTTGGATTAATGATGTAACCCAGAACCCCTCAATTTGTACTCTAGAAGGA 413
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  328 ataatgatttcagggccatagctaaactttcagattatcatggtctgtggccgagttcaga 387
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  414 GTACACAATTTCAAGAAATGGCTTAATTTTCAGAGATTATCATGCTTACCAGAGTTTCTAGA 473
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY  388 atgctgtggctaatttatggttagaacaagggggaacagaaatcacggtttgacccctgac 447
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QY 616 ataattttgttgcacaaaggaagcattggaagatgctctatgagaaagcaagagagat 675  
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QY 676 aacatcaagtaaaaggtttactatgacaccaatccatcaaatccattaggaacacatcatg 735  
Db 250 AATATCAAGTAAGGATTAATCTTATAACCAATCCATCAAAATCCATTAAGGTACAAATTTG 309  
QY 736 gacagaagacactgagaacccgtggtgagcttcacatgagaagcgtatccaccttgta 795  
Db 310 GACAGGAACATTAAGACATATTAAGATTCATCAATGACAAAACATACATCTAGTA 369  
QY 796 tctgtgaaatatactgcacagcttttcagccagccacccggtttcacaagcattagctgag 855  
Db 370 TGTGATGAATCTATGACGACACCCGCTTTAGTCAACCTTCATCAGTATCTCAGAA 429  
QY 856 atattagaggatgaacagacatagatgtagccgcaacctcgctacacattgtttatagt 915  
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Db 604 AGATTGATTGCTCAATGTTATTAGACACTATCTTTGNTGAAGATTTCATCCGGAAGAC 663  
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Db 664 TCGATGAG 671

RESULT 13  
BE555018  
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DEFINITION sp83q02.v1 Gm-cl045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
Gm-cl045-267 5' similar to SW:1A1C\_SOYBN P31531  
1-AMINOACYLCLOROPANE-1-CARBOXYLATE SYNTHASE ; , mRNA sequence.  
ACCESSION BE555018  
VERSION BE555018.1 GI:9819505  
KEYWORDS soybean.  
SOURCE Glycine max  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.  
REFERENCE 1 (bases 1 to 468)  
AUTHORS Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna  
,A., Bolla,B., Harris,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wylie,T., Underwood,K., Sceptoe,M., Theising,B., Allen,M., Bowers  
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
,R., Waterston,R. and Willson,R.  
Public Soybean EST Project  
Unpublished (1999)  
CONTACT: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel.: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu  
This clone is available through: ResGen, Invitrogen Corp. 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: ccu@resgen.com  
Insert Length: 913 Std Error: 0.00  
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FEATURES  
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XhoI; This cDNA library was constructed from mRNA isolated  
from etiolated hypocotyl tissue of 9-10 day old seedlings  
of the cultivar Williams 82. Complementary DNA was  
synthesized from mRNA using a primer consisting of a  
poly(dT) primer with a XhoI restriction site. EcoRI  
adapters were ligated to the blunt-ended cDNA fragments  
followed by digestion with EcoRI and XhoI. The cDNA  
fragments were directionally cloned into the EcoRI-XhoI  
restriction site of the pBluescript vector. The ligated  
cDNA fragments were transformed into DH10B host cells  
(Gibco BRL). This library was constructed by Dr. Randy  
Shoemaker."  
BASE COUNT 137 a 93 c 98 g 140 t  
ORIGIN  
Query Match 16.8%; Score 322.4; DB 10; Length 468;  
Best Local Similarity 89.5%; Pred. No. 9.3e-70;  
Matches 358; Conservative 0; Mismatches 41; Indels 1; Gaps 1;  
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QY 1277 atgtttcacctgctattctccattgcactgagccaggtggttaggtgctgctag 1336  
Db 64 ATGTTTCACCTGCCTCTTCTTCCATTTGCACAGCCAGGGTGGTTTAGGGTGTGCTATG 123  
QY 1337 ccaacatggatgatggctgtgcaaaattgcttggcaacgaatccgcaactttgtgcttc 1396  
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Db 184 AAAACAAGGAGGTCATGGTTCCTTAACAAGAAACATTTGCTGGCACAGATAACTTGA 243  
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Db 244 GCCTCAAAACCAAGAGTTTGATGATATCATGATGTCACCTCACCTCCCTATACCTCAGT 303  
QY 1517 cacttatggttaagccacaaattgagtttgcatattcctctgaaatcgt-ttagaagaag 1575  
Db 304 CCCCTTGGTTAAAGCCACAATTTGAGTTGCCATATTTCTCTGCACCATCTCAGAGAAG 363  
QY 1576 taactgatatggaagattacttggtttctttatttgta 1615  
Db 364 TAACATGATATACGATGATTATTTGGTTCTTTGATTGTTTA 403  
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DEFINITION EST243120 tomato ovary, TAMU lycopersicon esculentum cDNA clone  
CLED2NI19, mRNA sequence.  
ACCESSION AI484859  
VERSION AI484859.1 GI:4380230  
KEYWORDS EST.  
SOURCE Tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
REFERENCE 1 (bases 1 to 575)

**AUTHORS** Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,  
Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Roman,  
C.L., Nieman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley,  
S.D. and Giovannoni, J.  
**TITLE** Generation of ESTs from tomato carpel tissue  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.

**FEATURES** source  
1. .575  
/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
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/clone="cLED2N19"  
/tissue\_type="carpel"  
/dev\_stage="5 days pre-anthesis to 5 days post-anthesis"  
/lab\_host="Xl1-Blue MRF"  
/note="Vector: pBlueScript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and  
directionally cloned cDNA in vector Lambda Zap II with 5',  
and 3' ends located at the EcoRI and XhoI sites,  
respectively."

**BASE COUNT** 206 a 83 c 117 g 169 t  
**ORIGIN**  
Query Match 16.7%; Score 321.2; DB 9; Length 575;  
Best Local Similarity 72.5%; Pred. No. 2e-69; Indels 0; Gaps 0;  
Matches 416; Conservative 0; Mismatches 158;  
QY 203 ttatcccaagataatcctcaagctgttgatgcaaatgggtctgtgagaaatcagctta 262  
DB 1 TTATCCACACAAATCTTAATGGTGTATTCAATGGTGGTGGTGAATACAGCTTT 60  
QY 263 cctctgattggtgagattgataactgaacacccctgaagcctccattgcaactccag 322  
DB 61 GTTTGATTAAATTCAGAAATGATAGTCAACAAACCAAAAGCCTCAATTTGTACATATG 120  
QY 323 aaggaataaagtattcagggccatagctaaatttcagattatcatgtgtcgtccaggt 382  
DB 121 AAGGAGTTCAAGATTTCAAGATATCTGCTATTTTCAAGACTATCATGCTTCCAGAAAT 180  
QY 383 tcagaaatgctgtgctaaattttatgctagaacaggagggaacagaatcacgtttgacc 442  
DB 181 TTAGAAAGCAGTTGCAAGATTCTAGGAGAAAGTGAAGAGAGATAGATGATGATTCATC 240  
QY 443 ctgaccgtattgtcatgagcgttgaggccaccgagacacgaagtcactgcctttgtt 502  
DB 241 CAGAAAGAAATAGTTATGAGTGGAGAGCAACAGGAGCTCATGAAGTTTGGCATTTTGT 300  
QY 503 tggcagatccggcagggaattcttagtcccatccattcattcaggctttgaccggg 562  
DB 301 TGCTGATCTGTGTAGTCACTTCTAGTTCCTACACCATATATCCAGGATTTGATAGAG 360  
QY 563 atttgaggtagaagcaggaggttaaaactgttccagttatgtcgatagctcaaaatatt 622  
DB 361 ATTTGAGATGGAGACAGGAGTACAACTTTTCTGTGTTGTGAGAGTTCACAAAT 420  
QY 623 tctgttgacaaagggaagcattggaagatgcctatgagaaagcaagagaggataacatca 682  
DB 421 TCAAGGTAAACAAAGAGCCCTTGAAGAGACATATAGTAAGCTCAAGATCAAAATATCA 480  
QY 683 gactaagggtttactgatcaccaatccatcaaatccattaggcacaatcatggacagaa 742  
DB 481 AAGTAAAGGATTACTTATTAACAAATCCATCAATTCATTAGTACAAATTTTGGACAAGG 540  
QY 743 agacactgagaaccgtggtgagcttccatcaatga 776  
DB 541 AACATTAAGACATATTAAGATTTCATTCATGA 574

**RESULT** 15  
BI421967  
**LOCUS** BI421967  
**DEFINITION** BI421967 tomato callus, TAMU Lycopersicon esculentum cDNA clone  
EST532633 5' end, mRNA sequence.  
CLEC68H15  
**ACCESSION** BI421967  
**VERSION** BI421967.1  
**KEYWORDS** GI:15195965  
**SOURCE** EST.  
**ORGANISM** tomato.  
Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 819)  
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,  
Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S., Ronning,  
C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.  
Generation of ESTs from tomato callus tissue  
Unpublished (1999)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.  
**FEATURES** source  
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/clone="CLEC68H15"  
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/lab\_host="Xl1-Blue MRF"  
/note="Vector: pBlueScript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; supplier: Giovannoni laboratory; cLEC - Cotyledons  
of seedlings 7-10 days post-germination were excised, cut  
at both ends and placed on MS medium with no selection.  
Mixed callus was harvested at 25 and 40 days and included  
undifferentiated masses. Tomato Callus EST Library"

**BASE COUNT** 259 a 133 c 177 g 250 t  
**ORIGIN**  
Query Match 16.4%; Score 316.2; DB 10; Length 819;  
Best Local Similarity 63.5%; Pred. No. 3.8e-68;  
Matches 521; Conservative 0; Mismatches 288; Indels 12; Gaps 2;  
QY 697 ctgaccacatccatcaaatccattaggcacaatcatggacagaaagacactgagaaacc 756  
DB 1 CTTTATAAACAACTTCAAAATCCATTAGGTACTCTTCTTGACAAAGGACACACTCCGTGAC 60  
QY 757 gtggtgagcttcataatgagaagcggtatccaccctgtatgtgatgataatgtgcga 816  
DB 61 ATTGTAACGTTCACTCAACTCGAAACATCCATTTAGTAGTCGATGAATCTATGCTGCT 120  
QY 817 acagtttcagcaaccgggtttcataagcatagctgagatattagaggatgaacacagac 876  
DB 121 ACGGTGTTGATCAGCCCTAGATTCATCAGTGTCTCTGAAATAGTTGAGGAT-----ATG 174  
QY 877 atagagtgtgaccgcgcacacctcgtacacattgtttatagtcttcaaggacatggggttc 936  
DB 175 ATTGAATGCAACAAAGATTTGATCCATATAGTCTATAGCTTGTCTAAAGACTTGGGATTT 234  
QY 937 cctggtctgagctgcgcacatatactctacaatgatcgtggttaattgtgcacgc 996  
DB 235 CCAGGATTCAGAGTTGGAATTTGTTTACTCTGACACAGTACAGTAGTAAACATTTGCTAGA 294  
QY 997 aaagtgtcaagcttggattgggtgtcaacacacactcagttatcttttagcatgatgcta 1056

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Db 295 AAGATGTCAGCCTTTGGGTAGTTCAACTCAGACACACAACTTTGCTTGCAATCAATGTTG 354
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Db 355 TCTGATGAAGTATTCTATTCACAAATTCATTGCTGAGAGTTCCGAAAGACTCGGAGAAAGG 414
QY 1117 ttcaagggttttcaactggtgggttggccaaagtggcctaaagtgccttgcgaagcaatgct 1176
Db 415 CAGGGGATGCTTTACAAAAGGACTAGCAGAACTTGGAAATTAGTACATTTGAAAAGCAATGCT 474
QY 1177 ggtctattgtgtgatgatttaaggcaactctcctcaaaaagccaaacttgcgaactctgaa 1236
Db 475 GGTGTTGTTTTCTGGATGCAATTAAGGAGGCTCTTAAGAGCAACCAATTTGATAGTGAG 534
QY 1237 acggagctttggaagtttatcatcatgaagttaagatcaaatgtttcacctgggctattcc 1296
Db 535 TTAGAATTATGAGAAATTATTATCAATCAAGTGAACCTTAATGTGTTTCAACGAGGATGTTCA 594
QY 1297 ttccattgcactgagccaggttgggttgggttgctatgccaacatggatgatggt 1356
Db 595 TTTTCATTGCTTGAACCTCGTTGGTTTGAAGTTTGTAGAGTTTGTGTTGCAAAACATGGATGACGAGACG 654
QY 1357 gtgcaaatgtcttgcagcaatccgcaactttgtgcttcaaaaacaagg-----aggtc 1410
Db 655 ATGAGGATGCAATTAAGAGGATAAGTTACTTTGTGCTTCAGCCAAAGGACTTAACAAAC 714
QY 1411 gtgtgtcttaagaacaattgttggcacagtaacttgaggctgagcctcaaaaccaga 1470
Db 715 ATTGCTGCTATTAAAGAAACAATGCAGCAGGAGGAAACTTCAGATCAGCTTATCGTTTCGA 774
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Db 775 AGATGGGATCATGAGTTTCATGAACCTCACCAGCTCACTCTCC 815
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Search completed: August 21, 2002, 00:26:04  
Job time: 5655 sec







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Db 1621 AGAAGGTACATAAGTGTGATTTGTTCTTTGGAACCAATACAGGAATCTCTGATG 1680
Qy 1681 ttgtttgtgatcgccatcaatccagtgctcctacaagttgtgctgtcttcacgacgc 1740
Db 1681 TTGTTTGTGATCGGCATCACAATCCAGTGTCTTACAAGTTGTCTCTTCATGACGCC 1740
Qy 1741 cctcaactcttagggcattttttcttttttttttttttttttttttttttttttttt 1800
Db 1741 CCTTCAATCTTAGGGCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1800
Qy 1801 ttatagagctgtaagtgtatgttattgtttatcagaagatccaaaagatgctgttaactg 1860
Db 1801 TTTATAGAGTCTGTAAGTGTATTTGTTTATCAGAAGAGTCCAAAAGATGCTGTGAAATCTG 1860
Qy 1861 ctactgaattgttaactttcaattatgaataaattgttaataaaggtcttcaaatctatt 1920
Db 1861 CTACTGAATTGTAACTTCAATATGAATAAATGTTAATAAGGCTTCAAAATTCATT 1920
Qy 1921 tcc 1923
Db 1921 TCC 1923

RESULT 2:
GMCACCS1
LOCUS G.max mRNA for ACC synthase. 1789 bp mRNA linear PLN 11-MAY-1995
DEFINITION G.max mRNA for ACC synthase.
ACCESSION X67100
VERSION X67100.1 GI:18557
KEYWORDS ACC synthase.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 1789)
REFERENCE 1 (bases 1 to 1789)
AUTHORS Li, N.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-1992) N. Li, USDA/ARS Plant Mol Biol Lab, B-006
BARC West, Beltsville MD 20705, USA
REFERENCE 2 (bases 1 to 1789)
AUTHORS Liu, D., Li, N. and Mattoo, A.K.
TITLE Nucleotide sequence of soybean ACC synthase
JOURNAL Unpublished
FEATURES
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BASE COUNT 532 a 338 c 402 g 517 t

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## ORIGIN

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Query Match 70.9%; Score 1363.8; DB 8; Length 1789;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 147; Indels 2; Gaps 1;

Qy 77 acatacaccataggttttcaagcccgatggaccacaaactcccccttgttccaaagatggcta 136
Db 152 ACATAGACTATATGGGTTGATGATGGGACCAACTCAATTTGTTCTAAGATGGTCA 211
Qy 137 ttggggatggacatggcgaaatcaccacatacttttgatggatgaagccttatgatcaaa 196
Db 212 TCGGAGATGGACATGGTGAAGCATCACCATACTTTGATGGATGAAGGCTTATGATGAA 271
Qy 197 accctttcaccacagataaactcactaacggtgttatgcataatgggtttctgtcagaatc 256
Db 272 ACCCCTTTTCATCCCAAGAGAAATCCTAACGGGGTATTCCAAATGGTCTTCTGAGAAATC 331
Qy 257 agcttacctgtattgttgaaagatggatactgaacacacccctgaagcctccatttgc 316
Db 332 AGCTTACTCTTGATTTGGTTGAAGATTGGATACCTGAATAACCCAGAGGCCCTCCATTTCGA 391
Qy 317 ctccagaaggaataaattgatttcaggccatagctaaactttcaggattatcatgctcgg 376
Db 392 CACCAGAAGGAATAAATGATTTTCAGGCCATAGCTAACTTTTCAGGATTTATCATGGTCTGC 451
Qy 377 ccgagttcagaataatgctgtgctgctaaatttatggtagaacaaggggaaacagaatcacgt 436
Db 452 CCGAGTTTCAGAAATGCTGTGCTAAATTCATGGGTAGAACAAAGAGGAAACAGAGTCACGT 511
Qy 437 ttgacctgacctgattgtcatgagcgggtgagccacggagacacagcaagtcactgct 496
Db 512 TTGATCCTGACCGTATTGTCATGAGCGGTGGAGCAACTGGAGACACACCAAGTCACACTGCT 571
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Db 632 ACCGGGATTTGAGGTGGAGAACAGAGGAATTAACCTTTGTTCCAGTTATGTGCGATAGCTCAA 691
Qy 617 ataattcgtttcacaaaagacattggaagatgcctatgagaaacagagagagata 676
Db 692 ACAATTCAGTTGACAAAGCAAGCATTTGGAGATGCGTATGAGAAGCCCAAGAGGATA 751
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Qy 737 acagaagacactgagaacccgtgtgagcttcatcaatgagaagcgtatccaccttggat 796
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Qy 1037 atcttttagcatcatgctaaatgatgatgttctgtgagaggtttcttggcagagatg 1096

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Db 1112 ATCTTTTGGATCAATGCTAAATGATGAGTTTGTGNAAGTTTCTGGTAGAGAGTG 1171  
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Db 1292 ACCCAACGCTTACACTCTGAAATGGAGCTTGGAGAGTGATCATCTGATGAGGTTAAGATCA 1351  
QY atgtttccactggtctatccctcattgactgagccaggggtggtttgaggtggtctatg 1336  
Db 1352 ATGTTTCACTGGCTCCCTCTTCCATGTCACAGCCAGGGTGGTTTAGGCTGTGCTATG 1411  
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Db 1712 GCTTGAGTTTGTATTTTAAACAGCAGTAACAGGCAATGCTGATATGTTT 1764

RESULT 3  
VRACCSYN 1104 bp mRNA linear JUN 11-MAY-1995  
LOCUS V.radiata mRNA for 1-aminocyclopropane-1-carboxylate synthase  
DEFINITION (partial).  
ACCESSION Z11562  
VERSION Z11562.1 GI:22067  
KEYWORDS 1-aminocyclopropane-1-carboxylate synthase.  
SOURCE Vigna radiata.  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
1 (bases 1 to 1104)  
Arteca, R.N.  
Direct Submission  
Submitted (07-JAN-1992) Richard N. Arteca, Department of Horticulture, The Pennsylvania State University, 103 Tyson Building, University Park, PA, 16802, USA  
2 (bases 1 to 1104)  
Botella, J.R., Arteca, J.M., Schlagnhauser, C.D., Arteca, R.N. and Phillips, A.T.  
Identification and characterization of a full-length cDNA encoding for an auxin-induced 1-aminocyclopropane-1-carboxylate synthase from etiolated mung bean hypocotyl segments and expression of its mRNA in response to indole-3-acetic acid  
Plant Mol. Biol. 20 (3), 425-436 (1992)  
93043033 Location/Qualifiers

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BASE COUNT 311 a 212 c 277 g 304 t  
ORIGIN

## Query Match

Best Local Similarity 99.8%; Score 1099.8; DB 8; Length 1104;  
Matches 1101; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 235 caaatgggtctgtgagaatcagcttacctctgattggttggaagattggaactgaac 294  
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Db 61 AACCTGAGAGCTCCATTGTCACACTCAGAAAGAAATAATGATTTCAGGCCCATAGCTAAC 120  
QY 335 ttccaggattatcatggtctggtccaggttcagaaatgctggtgctaaatttatggctaga 414  
Db 121 TTTCAGGATTATCATGGTCTGGCCGAGTTTCAGAAATGCTGTGGCTAAATTTATGCTAGA 180  
QY 415 acaaggggaacagaaatcacgtttgacctgacctgattgcatgagcgggtggagccacc 474  
Db 181 ACAAGGGGAACAGAAATCACGTTTGACCTGACCGTATGTCATGAGCGGTGGAGCCACC 240  
QY 475 ggagcacacgaagcactgcctttgttggcagatcccgcgaggcattctttagtgcgc 534  
Db 241 GGACACACGAAAGTCACTGCTTTGTTGGCAGATCCGCGAGGCATTTCTTAGTGCCC 300  
QY 535 attccctattatccaggctttgaccggattgaggtggagaaacaggaggttaactgtt 594  
Db 301 ATTCCCTATTATCCAGGCTTTGACCGGATTTGAGGTGGAGACAGAGTTAAACTTGT 360  
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Db 421 TATGAGAAAGCAAGAGAGGATTAACATCAGAGTAAGGGTTTACTGATCAACATCATCA 480  
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QY 775 gagaagcgtaccacttgatgtgataatgataatctgctgcaacagtttccagcaacc 834  
Db 541 GAGAGCGTATCCACCTGTGTGATGATGAATATATGCTGCAACAGTTTTCAGCCAACCC 600  
QY 835 ggtttcataagcagctgagatattagagatgaaacagacagatagctgagccgaac 894  
Db 601 GTTTCAATAGCATAGCTGAGATATTAGAGGATGAACAGACATAGAGTGTGACCGCAAC 660

QY 895 ctgcacacattgtttatagctcttcaagacatgggttccctggcttcagagtcgc 954  
Db 661 CTGTAACATGTTTATAGTCTTTCAAGACATGGGTTCCTGGCTTCAGAGTCGGC 720  
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Db 721 ATCATATACTTTACAAATGATGCTGGTTAATGTGCACGCAAAATGTCAAGCTTTTGA 780  
QY 1015 ttggtgtcaacacagactcagtatcttttagcatcagatcgaatgatgagtttgc 1074  
Db 781 TTGGTGTCAACACAGACTCAGTATCTTTTAGCATCGATGCTAATGATGATGATTTGTG 840  
QY 1075 gagaggtttctgcagagagtgcaagaggtgtgctcaaggttcaggttttccactggg 1134  
Db 841 GAGAGGTTTCTGCAGAGAGTGCAAGAGGTTGGCTCAAGGTTTCAGGTTTCACATGGG 900  
QY 1135 ggtgtgccaagtgtgcataaagtctgcgaagcaatgctggtctatttgtgtgagtg 1194  
Db 901 GGCTTGGCCAAAGTTGGCAATGCTTGCAAAGCAATGCTGCTATTTGTGTGGATG 960  
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Db 1021 ATCATTCATGAAGTTAAGATCAATGTTTCACTGGCTATTCCTTCATGCACTGAGCCA 1080  
QY 1315 ggtgtgttaggtgtgctatgc 1337  
Db 1081 GGCTGCTTCAGGCTGCTTTGC 1103

RESULT 4  
LOCUS AY062022  
DEFINITION Medicago truncatula 1850 bp mRNA linear PLN 03-DEC-2001  
ACCESSION AY062022  
VERSION AY062022.1 GI:17266327  
KEYWORDS  
SOURCE Medicago  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
REFERENCE 1 (bases 1 to 1850)  
AUTHORS Engstrom,E.M. and Long,S.R.  
TITLE MtACC synthase, a putative 1-aminocyclopropanecarboxylic acid  
synthase from Medicago truncatula  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1850)  
AUTHORS Engstrom,E.M. and Long,S.R.  
TITLE Direct Submission  
JOURNAL Submitted (13-NOV-2001) Biological Sciences, Stanford University,  
371 Serra Mall, Stanford, CA 94305-5020, USA  
FEATURES  
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BASE COUNT 580 a 294 c 361 g 615 t  
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Best Local Similarity 79.0%; Pred. No. 2.4e-243;  
Matches 1217; Conservative 0; Mismatches 307; Indels 17; Gaps 3;  
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 Pism sativum 1849 bp mRNA linear PLN 23-JUL-2001  
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 KEYWORDS  
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 ORGANISM  
 Pism sativum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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 Pism.  
 1 (bases 1 to 1849)  
 Peck, S.C. and Kende, H.  
 A gene encoding 1-aminocyclopropane-1-carboxylate (ACC) synthase  
 produces two transcripts: elucidation of a conserved response  
 Plant J. 14 (5), 573-581 (1998)  
 MEDLINE  
 PUBMED  
 98340552  
 9675901  
 2 (bases 1 to 1849)  
 Peck, S.C. and Kende, H.  
 Differential regulation of genes encoding  
 1-aminocyclopropane-1-carboxylate (ACC) synthase in etiolated pea  
 seedlings: effects of indole-3-acetic acid, wounding, and ethylene  
 Plant Mol. Biol. 38 (6), 977-982 (1998)  
 9908479  
 MEDLINE  
 REFERENCE  
 3 (bases 1 to 1849)

AUTHORS Peck, S.C. and Kende, H.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-JUL-1997) MSU-DOE Plant Research Laboratory, Michigan  
 State University, Plant Biology Building, East Lansing, MI  
 48824-1312, USA

FEATURES  
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BASE COUNT 580 a 325 c 378 g 566 t

Query Match 48.6%; Score 935; DB 8; Length 1849;  
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RESULT 6  
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LOCUS  
DEFINITION  
AB034992 1980 bp mRNA linear PLN 09-MAR-2000  
Malus domestica MdACS-5A mRNA for 1-aminocyclopropane-1-carboxylate  
synthase, complete cds.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AB034992.1 GI:7209850  
1-aminocyclopropane-1-carboxylate synthase.  
Malus domestica cDNA to mRNA.  
Malus x domestica  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
AB034992  
Submitted (16-NOV-1999) Takeo Harada, Hirosaki University, Faculty  
of Agriculture and Life Science, Bunkyocho 3, Hirosaki, Aomori  
036-8561, Japan (E-mail:tharada@cc.hirosaki-u.ac.jp,  
Tel:81-172-39-3777, Fax:81-172-39-3750)  
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Query Match 41.5%; Score 797.6; DB 8; Length 1980;  
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QY	1523	tggttaaagc	1532
Db	1513	TACCTCAATC	1522
RESULT	7		
LOCUS	E12805		
DEFINITION	CDNA encoding poplar ACC (1-aminocyclopropane-1-carbonic acid) synthetase which is induced by ozone.		
ACCESSION	E12805		
VERSION	E12805.1	GI:3251637	
KEYWORDS	JP 1997075088-A/1.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 1864)		
AUTHORS	Hoya,I.I. and Kitani,S.		
TITLE	OZONE-DERIVED 1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID-SYNTHESIZING ENZYME GENE GROUP OF WOODY PLANT.		
JOURNAL	Patent: JP 1997075088-A 1 25-MAR-1997;		
COMMENT	TOYOTA MOTOR CORP		
	OS Populus nigra L. (poplar)		
	PN JP 1997075088-A/1		
	PD 25-MAR-1997		
	PF 07-SEP-1995 JP 1995254510		
	PI HOYA IZUMI, KITANI SHIGEKAZU		
	PC C12N15/09,C07H21/04,C12N9/88//A01H5/00,(C12N9/88,C12R1:19); CC		
	strandedness: Double;		
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	CC hypothetical: No;		
	CC anti-sense: No;		
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	FT 5'UTR	/clone='pPNA CCS1'	
	FT CDS	1. .193	
	FT	194. .1639	
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	which is induced by ozone' FT	cyclopropane-1-carbonic acid) FT	
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Best Local Similarity	73.0%;	Pred. No. 3.6e-193;	Length 1864;
Matches 1047;	Conservative	0;	Mismatches 378;
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			Gaps 2;
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QY	170	ttgatggatggaagccttatgatcaaaacccctttccatccacagataatccctaacgggtg	229
Db	270	TCGATGGCTGGAAAGCCTATGACAGTGTATCCCATCATCCACGGACAATCCAAATGGAG	329
QY	230	ttatgcaaatgggtcctgtcgtgagaatacagcttacccttgatttggttgatgtgatac	289
Db	330	TTATCCAGATGGGTCTTCGAGAGAAATCAGCTGTGCTTGATTTGATTCAGACTGGCTCA	389





QY 170 ttgatgagtggaaggccttctgatcaaaaccccttttccatccacagataaatccctacaggtg 229  
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RESULT 9  
 AB034993  
 LOCUS  
 DEFINITION Malus domestica MdACS-5B mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds.  
 ACCESSION AB034993  
 VERSION AB034993.1 GI:7209852  
 KEYWORDS 1-aminocyclopropane-1-carboxylate synthase.  
 SOURCE Malus domestica cDNA to mRNA.  
 ORGANISM Malus x domestica  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
 REFERENCE 1 (sites)  
 AUTHORS Sunako,T., Ishikawa,R., Senda,M., Akada,S., Niiizeki,M. and Harada,T.  
 TITLE MdACS-5A (Accession No. AB034992) and 5B (Accession No. AB034993), two wound-responsive genes encoding 1-aminocyclopropane-1-carboxylate synthase in apple. (PGR00-030)  
 JOURNAL Plant Physiol. 122, 620 (2000)  
 REFERENCE 2 (bases 1 to 1838)  
 AUTHORS Harada,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-1999) Takeo Harada, Hirosaki University, Faculty of Agriculture and Life Science, Bunkyocho 3, Hirosaki, Aomori 036-8561, Japan (E-mail:tharada@cc.hirosaki-u.ac.jp, Tel:81-172-39-3777, Fax:81-172-39-3750)

FEATURES  
 Location/Qualifiers  
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BASE COUNT 528 a 371 c 412 g 527 t  
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RESULT 10

AF386523

LOCUS

DEFINITION

Pyrus communis 1-aminocyclopropane 1-carboxylate synthase 5 (ACS5)

VERSION

AF386523.1

KEYWORDS

GI:18252346

SOURCE

Pyrus communis

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.

REFERENCE

1 (bases 1 to 1770)

El Sharkawy, I., Li, Z. G., Latche, A. and Lelievre, J. M.

Ripening related genes in pear (Pyrus communis)

JOURNAL

Unpublished

AUTHORS

2 (bases 1 to 1770)

El Sharkawy, I., Li, Z. G., Latche, A. and Lelievre, J. M.

TITLE

Direct Submission

JOURNAL

Submitted (30-MAY-2001) Biologie Molculaire et Physiologie de la Maturation des Fruits, INP - ENSAT, Av. de l'Agrobiopole - BP107, Castanet Tolosan Cedex 31326, France.

FEATURES

source

1..1770

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/db\_xref="taxon:23211"

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172..1635

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BASE COUNT 493 a 381 c 418 g 478 t

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Best Local Similarity 72.5%; Pred. No. 6.5e-190;  
Matches 1051; Conservative 0; Mismatches 389; Indels 9; Gaps 3;

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## RESULT 11

CSIO12551 1734 bp mRNA linear PLN 26-JAN-2000

LOCUS Citrus sinensis mRNA for ACC synthase.

DEFINITION AJ012551

ACCESSION AJ012551

VERSION AJ012551.1 GI:6433835

KEYWORDS ACC synthase; ACS1 gene.

SOURCE Citrus sinensis.

ORGANISM Citrus sinensis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

REFERENCE 1 (bases 1 to 1734)

AUTHORS Wong, W.S., Ning, W., Xu, P.L., Kung, S.D., Yang, S.F. and Li, N.

TITLE Identification of two chilling-regulated 1-aminocyclopropane-1-carboxylate synthase genes from citrus (Citrus sinensis Osbeck) fruit

JOURNAL Plant Mol. Biol. 41 (5), 587-600 (1999)

MEDLINE 20108317

REFERENCE 2 (bases 1 to 1734)

AUTHORS Wong, W.S.

TITLE Direct Submission

JOURNAL Submitted (10-NOV-1998) Wong W.S., Biology, The Hong Kong University of Science and Technology, Rm.6207, Biology Department, HKUST, Clear Water Bay, Kowloon, HONG KONG

FEATURES

Location/Qualifiers

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DEFINITION  
ACCESSION U68216  
VERSION U68216.1 GI:4090534  
KEYWORDS  
SOURCE papaya.  
ORGANISM Carica papaya  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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Rosidae; eurosids II; Brassicales; Caricaceae; Carica.  
REFERENCE  
AUTHORS Neupane, K.R., Mukatira, U.T. and Stiles, J.I.  
TITLE Cloning of Fruit-Specific ACC Synthase and ACC Oxidase cDNAs From  
Papaya (Carica papaya L.) and Their Expression During Fruit  
Ripening  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1888)  
AUTHORS Neupane, K.R., Mukatira, U.T. and Stiles, J.I.  
TITLE Direct Submission  
JOURNAL Submitted (28-AUG-1996) Plant Molecular Physiology, College of  
Tropical Agriculture and Human Resources, University of Hawaii,  
3190 Malle Way, St John #503, Honolulu, HI 96822, USA  
FEATURES  
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JOURNAL Submitted (07-FEB-1997) Horticulture, Pennsylvania State University, 102 Tyson Building, University Park, PA 16802, USA  
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E12806  
LOCUS  
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ACCESSION E12806  
VERSION E12806.1 GI:3251638  
KEYWORDS JP 199705088-A/2.  
SOURCE unidentifed.  
ORGANISM unclassified.



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REFERENCE 1 (bases 1 to 1868)
AUTHORS Hoya, I. and Kitani, S.
TITLE OZONE-DERIVED 1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID-SYNTHESIZING
JOURNAL ENZYME GENE GROUP OF WOODY PLANT
PATENT Patent: JP 1997075088-A 2 25-MAR-1997;
COMMENT TOYOTA MOTOR CORP
OS Populus nigra L. (poplar)
PN JP 1997075088-A/2
PD 25-MAR-1997
PF 07-SEP-1995 JP 1995254510
PI HOYA IZUMI, KITANI SHIGEKAZU
PC C12N15/09, C07H21/04, C12N9/88, A01H5/00, (C12N9/88, C12R1.19); CC
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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FT (1-aminocyclopropane-1-carbonic acid) FT
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## RESULT 15

AB033503

LOCUS

DEFINITION

AB033503

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AB033503 1868 bp mRNA linear PLN 15-APR-2000  
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AB033503.1 GI:7576443

1-aminocyclopropane-1-carboxylate synthase.

Populus euramericana (cultivar:I-45/51) cDNA to mRNA.

Populus euramericana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.

1 (sites)

Koch, J.R., Minocha, R., Nakajima, N., Yasutani, I., Saji, H.,

Rebeck, J. and Davis, K.R.

Induction of ethylene and putrescine by ozone: Comparison of an



JOURNAL	orzone-sensitive and an ozone-tolerant hybrid popular clone
REFERENCE	Unpublished (1999)
AUTHORS	2 (bases 1 to 1868) Nakajima,N., Yasutani,I., Koch,J.R., Minocha,R., Saji,H., Rebeck,J. and Davis,K.R.
TITLE	Direct Submission
JOURNAL	Submitted (12-OCT-1999) Nobuyoshi Nakajima, The National Institute for Environmental Studies, Regional Environment Division; Onogawa 16-2, Tsukuba, Ibaraki 305-0053, Japan (E-mail:naka-320@nies.go.jp, Tel:81-298-50-2490, Fax:81-298-50-2490)
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9: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2559	100.0	484	21	AA179292
2	1881.5	73.5	481	18	AAW21754
3	1875.5	73.3	490	19	AAW60235
4	1823	71.2	487	19	AAW57484
5	1771.5	69.2	483	22	AAE00986
6	1771.5	69.2	483	22	AAE59724
7	1765	69.0	504	19	AAW52818
8	1762.5	68.9	483	12	AAW15509
9	1762.5	68.9	486	18	AAW21755
10	1755.5	68.6	485	22	AAE00985
11	1755.5	68.6	485	22	AAE59723

12	1746.5	68.2	485	12	AAE15508
13	1713	66.9	485	12	AAE15507
14	1713	66.9	485	19	AAW47314
15	1713	66.9	485	22	AAE00984
16	1713	66.9	485	22	AAE59720
17	1713	66.9	485	22	AAE59725
18	1710	66.8	485	12	AAE15506
19	1710	66.8	485	19	AAW47313
20	1710	66.8	485	22	AAE00983
21	1710	66.8	485	22	AAE59719
22	1702.5	66.5	482	19	AAW60234
23	1698.5	66.4	482	19	AAW60233
24	1696	66.3	485	19	AAW39422
25	1676.5	65.5	482	18	AAW09878
26	1637.5	64.0	390	18	AAW09879
27	1637.5	64.0	493	12	AAE15504
28	1637.5	64.0	493	19	AAW47310
29	1637.5	64.0	493	22	AAE00980
30	1637.5	64.0	493	22	AAE59716
31	1636.5	64.0	493	12	AAE15505
32	1636.5	64.0	493	19	AAW47311
33	1636.5	64.0	493	22	AAE00981
34	1636.5	64.0	493	22	AAE59717
35	1636.5	64.0	493	22	AAE59721
36	1633.5	63.8	493	13	AAE25406
37	1627.5	63.6	494	12	AAE15863
38	1627.5	63.6	494	19	AAW47312
39	1627.5	63.6	494	22	AAE00982
40	1627.5	63.6	494	22	AAE59718
41	1627.5	63.6	494	22	AAE59722
42	1603.5	62.7	517	17	AAW04558
43	1573	61.5	496	15	AAE53114
44	1563	61.1	476	22	AAE00988
45	1563	61.1	476	22	AAE59727

#### ALIGNMENTS

RESULT 1

AA179292

ID AA179292 standard; Protein; 484 AA.

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DT 03-JUL-2000 (first entry)

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Isolated nucleic acid molecule for producing transgenic plants having altered characteristics such as resistance to a plant pathogen comprises promoter, inducible in response to physical stimulation -

5

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PS Claim 4iv; Page 101-103; lllpp: English.
XX
CC The present sequence is that of 1-aminocyclopropane-1-carboxylic
CC acid synthase (ACC synthase) of mung bean. ACC synthase expression
CC is induced in response to mechanical strain, auxin and salt stress.
CC The invention relates to the promoter, pGEL-1 (see AA294266), of the
CC ACC synthase gene, AIM-1. pGEL-1 is capable of induction by
CC physical and/or environmental stimuli in cells in which it is
CC indigenous and, in the absence of any negative regulatory mechanism,
CC is capable of constitutive expression in cells in which it is
CC non-indigenous. The promoter can be used to direct expression of
CC genes conferring useful traits on plants, such as improved
CC resistance to a plant pathogen, altered nutritional characteristics,
CC expression of a plant body, altered biochemical pathway, altered
CC fertility, and/or altered flower colour.
XX
SQ Sequence 484 AA;

Query Match 100.0%; Score 2559; DB 21; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.6e-247;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFKAMDQTPLLSKAIGDGHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTS 60
DB 1 mgykamdqtpllskmaigdgghgesspyfdgwkaydqpnhptdnpngvmqglanqlts 60
QY 61 DLVEDWILNPNASICTPGINDFRAIANFODYHGLAEFRNAVAKFMARTGRNRTFDPD 120
DB 61 dlvedwilnpeasictpegindefraianfodhyglaefrnavakfmartgrnrtfdpd 120
QY 121 RIVMSGGATGAHEVTAFCIADPGEAFIPYYPGDFDRDLRWRTGVKLVPMVCDSSNNFV 180
DB 121 rivmsggatgahvtafciaadpgeafipypgdfdrdlrwtgkvlvpmcdssnnfv 180
QY 181 LRKEALEDAYEKAREDNIRVKGILLTNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDBI 240
DB 181 lrkealedayekarednirvkgilltnpsnplgtimdrktrlrtvvsfinekrihlvcdbi 240
QY 241 YAATVFSQPGFTISAEILDETDIECDRLNVHIVYSLSKDMGFPGRFVGIYISYNDVAVN 300
DB 241 yaatvfsqpgftisaeildecdrnlvhlvyslskdmgfpgrfvgiylsyndavvn 300
QY 301 CARKMSSFGVSTQTYQLASMLNDEFVERFLAESAKRLAQRFVFTGGLAKVGKICLQ 360
DB 301 carkmssfgvstqtyqlasmlndefverflaesakrlaqrfvftgglakvgkiclq 360
QY 361 SNAGLEFVWMDLRLKLPFTFSETELWKVIIHEVKINSPGYSFHCTEPGWFRVCYANMD 420
DB 361 snaglefvwmdlrlklpftfsetelwkviilhevkinvspgysfhtepgwfrvcyanmd 420
QY 421 DMAVQIALQIRNFVLQNKVVVSNKKHCWHSNLRSLKTRFRDDITMSPHSPPLQSPMV 480
DB 421 dnavqialqirnfvlqnkvvvsunkhchwshsnlrslktrfrdditmsphspplqspmv 480
QY 481 KATN 484
DB 481 katn 484

RESULT 2
AAW21754
ID AAW21754 standard; Protein; 481 AA.
XX
AC AAW21754;
XX
XX 26-AUG-1997 (first entry)
DE Poplar 1-aminocyclopropane-1-carboxylic acid synthase PNACCS1.
XX
XX Ozone; induction; exposure; resistance; transgenic plant; ACC1;
KW 1-aminocyclopropane-1-carboxylic acid biosynthesis.
XX
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OS Poplar nigra.
XX
PN JP09075088-A.
XX
PD 25-MAR-1997.
XX
PF 07-SEP-1995; 95JP-0254510.
XX
PR 07-SEP-1995; 95JP-0254510.
XX
PA (TOYT ) TOYOTA JIDOSHA KK.
XX
DR WPI; 1997-239270/22.
DR N-PSDB; AAT73501.
XX
PT Ozone-induced 1-amino-cyclopropane-1-carboxylic acid synthetic
PT enzyme genes - from poplar tree, are useful for generating
PT ozone-resistant trees and pollution clean-up trees
XX
PS Claim 2; Pages 7-9; 12pp: Japanese.
XX
CC This protein is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase
CC encoded by a cDNA clone isolated from poplar trees which
CC had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone
CC for 6 hours after one hour acclimation at 25 degrees C, 70 % relative
CC humidity, 30 k lux and air current 30 cm/second. The gene will be
CC useful for breeding air pollutant ozone-resistant trees, especially
CC poplar.
XX
SQ Sequence 481 AA;

Query Match 73.5%; Score 1881.5; DB 18; Length 481;
Best Local Similarity 73.5%; Pred. No. 1.3e-179;
Matches 349; Conservative 58; Mismatches 65; Indels 3; Gaps 2;

QY 11 LLSKMAIGDGHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTSLDVEDWILNN 70
DB 9 llskmaigdgghgesspyfdgwkaydqpnhptdnpngvlgmglanqlcfdliqdwllkn 68
QY 71 PRASICTPGINDFRAIANFODYHGLAEFRNAVAKFMARTGRNRTFDRIVMSGGATG 130
DB 69 prasicspgelnfreaiafgydhyglpefrnavanmekvrgnrvctfdpdrivmsggatg 128
QY 131 AHEVTAFCIADPGEAFIPYYPGDFDRDLRWRTGVKLVPMVCDSSNNFVLTKAELEDAY 190
DB 129 ahetiafciadpgeafipypgdfdrdlrwtgkvlipvdsdsannfmvtrealenay 188
QY 191 EKAREDNIRVKGILLTNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDIYATVFSQPG 250
DB 189 ekaqldnirkvgilltnpsnplgtildretlrsivfinekrihlvcdelyaatvfsqpd 248
QY 251 FTSIAEILDETDIECDRLNVHIVYSLSKDMGFPGRFVGIYISYNDVAVNCARKMSSFGL 310
DB 249 flsvrrillge--diecnldvlhivyslskdmgfpgrlrvgllysyndavvscarkmssfgl 306
QY 311 VSTQTYQLASMLNDEFVERFLAESAKRLAQRFVFTGGLAKVGKICLQ-SNAGLEFVW 369
DB 307 vstqtyqlasmlsdnefverfleaesakrlaaryrvtgldvgieclksnagiflwm 366
QY 370 DLRLKLPFTFSETELWKVIIHEVKINSPGYSFHCTEPGWFRVCYANMDMAVQIALQ 429
DB 367 dslrllkqtkfaemalwrviilhevkinvspgcsfclkpqgwfrvcfannmdetcmqvals 426
QY 430 RIRNFVLQNKVVVSNKKHCWHSNLRSLKTRFRDDITMSPHSPPLQSPMVKATN 484
DB 427 riktfnvkeadtcksrknlrwgsgllksprlyddfnshpspibpqsplvrarn 481

RESULT 3
AAW60235
ID AAW60235 standard; Protein; 490 AA.
XX
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	Best Local Similarity	70.98	Pred. No. 9.7e-174						
	Matches	339	Conservative	65	Mismatches	66	Indels	8	Gaps
Qy	11	LLSKMAIGDHGESSPYFDGKWKAYDQNPFTDPNPGVMQGLAENQLTSLDVEDWILNN	70						
Db	10	llskiatenghgedspsyfdgwkaydsdphtqpevgiqmglaenqlcfnlihwllkn	69						
Qy	71	PEASICTPEGINDFRATIANFODYHGLAEFRNAVAKFMARTGRNRTITDPDRIYVMSGGAT	130						
Db	70	peasictaqgaefrtalfqdyhglaefreavafmgkvrrnrasfddpdrivmsggatg	129						
Qy	131	AHEVTATCLADPGGAFLPIPIYYPGFDRLDWRRTGVKLVPPVCDSSNFFVLTKALEDAY	190						
Db	130	ahematacladpgdafivptpyyfgdrldrtwrtgkvklipvccssndyqitaeleay	189						
Qy	191	EKAREDNRVKGLLITNPSNPLGIMDRKTLRTVVSFINEKRIHLVCDIYAATVFSOPG	250						
Db	190	etageadkivkgllippsnplgtiitkdtleavftfnhknhlhvcdieyaatvfsgpe	249						
Qy	251	FISTAILEDTEIDECORNLVHIYVLSKDMGPFGRVGIITYSYNDAYVNCARKMSSFGL	310						
Db	250	ftsiaelle-edkiccnrdllhiysltekdmgpgfrvgivsyndavvscarkmssfgl	308						
Qy	311	VSTOTVYLLASMLNDDVEVERFLAESAKRIAQRVRVFTGGLAKVGICLQSNAGLIVVMD	370						
Db	309	vssqtqyliasmldadefvdfgivesrkrldmrhsfftqrlaqvginclkenagifvmd	368						
Qy	371	LROLLLKPTDFSETELMKVIITHEKINYSFGYSFHCTEPGFVRVCYANNDDMAVOIALQR	430						
Db	369	lrrlllkeqtfeamvwlrvlineaklnvsgssfcscpgvfrvcfamdkdmeialsr	428						
Qy	431	IRNPVLQNEVVVGNKKHCWHSNLRLSUKTRRFDIT-----MSPHPLPQSPMVKA	482						
Db	429	iktfmllqkeamvpkklcwtsrlrfsfs-rvedlmetpsfmsfpicqslvira	485						

RESULT	5	
AAE00986		
ID	AAE00986	standard; Protein; 483 AA.
XX		
AC	AAE00986;	
XX		
DT	04-JUL-2001	(first entry)
XX		
DE	Tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC 1B.	
XX		
KW	Tomato; 1-aminocyclopropane-1-carboxylic acid synthase; LE-ACC 1B;	
XX	ethylene production; fruit ripening; transgenic plant.	
OS	Lycopersicon esculentum.	
XX		
PN	US6207881-B1.	
XX		
PD	27-MAR-2001.	
XX		
PF	25-JAN-1995;	95US-0378313.
XX		
PR	19-APR-1992;	92US-0862493.
PR	10-SEP-1990;	90US-0579896.
XX		
PA	(USDA )	US SEC OF AGRIC.
XX		
PI	Theologis A, Sato T;	
XX		
DR	WPI; 2001-289591/30.	
XX		
PT	Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic	
PT	acid synthase, LE-ACC2 useful for producing ACC synthase which is	
PT	essential for the production of ethylene in higher plants -	
XX		
PS	Example 3; Fig 10; 92pp; English.	
XX		
CC	The present sequence is tomato 1-aminocyclopropane-1-carboxylic acid	

synthase, LE-ACC 1b. ACC synthase are capable of catalysing the conversion of ADOMET (S-adenosyl methionine) to ACC and methyl thioadenosine (MTA). ACC DNA is useful for producing ACC synthase which is essential for the production of ethylene in higher plants, where ethylene is a determinant of fruit ripening. The ACC DNA is also useful for producing transgenic plants which are overproducers of or are deficient in ACC synthase.

Sequence 483 AA;

	Query Match	69.2%;	Score 1771.5;	DB 22;	Length 483;
	Best Local Similarity	68.9%;	Pred. No. 1.4e-168;		
	Matches 326;	Conservative 76;	Mismatches 66;	Indels 5;	Gaps
Qy	11	LLSKMAIGDGHGESSPYFDGKAYDQNPFPHTDPNPGVMQGLAENOLTSLPVEDWILN	70		
Db	13	llskiatndngensnpyfdgwakayannpfhtdntpgvimglaenlcfolligemvnn	72		
Qy	71	PEASICTPEGINDPRAIANFODYHGLAEFRNAVAKEMARTGNRITDPDRIVMSGGATG	130		
Db	73	pkaasictvegaenfqdaifgdqyhglpesfrqavarfemkvegrdvtfqpnrvmsggatg	132		
Qy	131	AHEVTAFCIADPGGEAFLPIPIYPYPCFDRDLRWRTGKVLVPVCMDOSSSNFVLTKEALEDAY	190		
Db	133	ahemlafciadpggdailvptpyppgdrdlrwtgvgqlfpvvcscndkfvttkaleeay	192		
Qy	191	EKARDNTRVRKGLLITNPSNPLGTIMDRKTLTRVVVSFINEKRIHLVDEIYAAVTFSPQG	250		
Db	193	ekaqgsnikikgllinnpsnplgtllldktdirdvtfinsknhlvdcelyaavtfqdpqr	252		
Qy	251	FISIAEILEDTEIDCDRLNVHIVYSKDMGFFGFRVGIITYSYNDVAVNCAKMSFFGL	310		
Db	253	fisvsemveem--tecntdlhivyslksdligfpgrvlgvysyndtvnlrsmssfgl	310		
Qy	311	VSTQTYQLLASLWLNDDFEVERFLAESAKRLAQRFRVFTGGLAKVGIKCLOSNAGLFVWMD	370		
Db	311	vstqtdqhmiasmlsdeifvekfiaesserlgrkgdmfckglagvgistlksnagllftwmd	370		
Qy	371	LRQLLKPTFDSEFELMKWVIIEYKVINSPGYSFCHTEPGWFRVCYANMDDMAVQIALQR	430		
Db	371	lrrlllkeatfdgelelwrliinevklvnspgscfhcsepqgvrvcfanmddetmrlarr	430		
Qy	431	IRNFVJQWKEV--VVSNNKKHCWHNLRSLKTRFRPDDITMSPHSPQLPQSPMWK	481		
Db	431	lrnfvlqtkglnnlaalkkqcsrkqlglsfrladdfnsphagmp-nepvlv	482		

RESULT	6
AB59724	Tomato ACC synthase gene LE-ACC1B(b) clone.
AA059724 standard; Protein; 483 AA.	ACC synthase; 1-aminocyclopropane-1-carboxylic ethylene production; fruit ripening; tomato
XX	Lycopodium obscurum.
US6156956-A.	
05-DEC-2000.	
02-MAR-1998;	98US-0033349.
25-JAN-1995;	95US-0378313.
02-APR-1992;	92US-0862493.
07-JUN-1995;	95US-0481171.
10-SEP-1990;	90US-0579896.

XX (USDA ) US DEPT OF AGRICULTURE.  
 XX Sato T, Theologis A;  
 XX WPI; 2001-079558/09.  
 XX Expression cassette for producing transgenic plants exhibiting  
 PT inhibited ethylene production and delayed fruit ripening, comprises  
 PT complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic acid  
 PT synthase synthesis -  
 XX Example 3; Fig 10; 91pp; English.  
 XX 1-aminocyclopropane-1-carboxylic acid (ACC) synthase is essential for  
 CC the production of ethylene in higher plants; ethylene is a determinant  
 CC of fruit ripening. The present invention relates to an expression  
 CC cassette which comprises the reverse transcript of RNA complementary to  
 CC an RNA transcribed from ACC synthase gene. The expression cassette can be  
 CC used to prevent ACC gene expression. The expression cassette is useful  
 CC for inhibiting ethylene production and fruit ripening, when introduced  
 CC into a plant or plant cells. The present sequence is the protein encoded  
 CC by tomato ACC synthase gene LE-ACC1B(b) clone. This sequence was used in  
 CC a sequence homology comparison with other ACC synthase gene clones  
 CC (AAB59721-B59727).  
 XX Sequence 483 AA;  
 SQ

Query Match 69.2%; Score 1771.5; DB 22; Length 483;  
 Best Local Similarity 68.9%; Pred. No. 1.4e-168;  
 Matches 326; Conservative 76; Mismatches 66; Indels 5; Gaps 3;  
 QY 11 LLSKMAIGDGHGSSPYFDGKAYDQNPFPHTDNPNGVMQGLAENQLTSDLVEDWLN 70  
 Db 13 llskmatndghenspyfdgkayannpfltdnptvigmqlaenqlctdlleewmn 72  
 QY 71 PEASICTPEGINDFRATANFDYHGLAEFRNAVAKFMRGRNRTFDPDRIVMSGATG 130  
 Db 73 pkasictvegaenfqdlaifqdyhgipefrqavarmekvrgdrvtfdpnrvmsgatg 132  
 QY 131 AHEVTAFLADPGEAFVLPIPPYPGFDRDLRWRTGKLVPMVMDSSNNFVLTKEALRDAY 190  
 Db 133 ahemlafcladpdafivptpypgfdrlwrtgqlfpvcescndfvtkaeay 192  
 QY 191 EKARENIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCEIYAATVFSQPG 250  
 Db 193 ekaqgsnikikllinnpsnplgtltdktldrtvtfinsknhlvceiyaatvfdqpr 252  
 QY 251 FISTAEITLEDTECDRLNHLVIVSLSKDMGPPGFRVGIYISYNDVAVNCARKMSFGL 310  
 Db 253 fivsvemveem--lecnldihivyslskdgtfpgfrvgyvgyndvtvnsrkmsfgl 310  
 QY 311 VSTQVOTYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGIAGVIGKICLQSNAGLFWMD 370  
 Db 311 vstqtqhmiasmdelifevkefaesserlgkqgmftkqlagvgistlksnaglfvmd 370  
 QY 371 LRQLLKPTFDESELMKVYIIEVKINVSFGYFHCTEPGWFRVCYANMDMAVQIALQR 430  
 Db 371 lrrllkeatfdgelelwrliinevklvnsfgcsfhosepgwfrvcvfanmdmetrialr 430  
 QY 431 IRNFVLQNKVEV--VVSNNKHCWNSNLRSLKTRFRDDITMSPHSPLPQSPMKV 481  
 Db 431 irnfvlqtknlnlaaikkcsrskqisrlsrllddfnspahspm--nslplr 482

RESULT 7  
 AAW52818  
 ID AAW52818 standard; Protein: 504 AA.  
 XX  
 AC AAW52818;  
 CC  
 DT 07-JUL-1998 (first entry)

XX Coffee-fruit specific ACC synthase.  
 DE  
 XX Coffee-fruit; 1-aminocyclopropane-1-carboxylic acid synthase;  
 KW ACC synthase; ethylene biosynthesis; fruit ripening.  
 XX Coffea arabica.  
 XX WO9806852-A1.  
 XX 19-FEB-1998.  
 XX 11-AUG-1997; 97WO-US14184.  
 XX 12-AUG-1996; 96US-0695412.  
 XX (UYHA-) UNIV HAWAII.  
 XX Moisyadi I, Neupane KR, Stiles JI;  
 XX WPI; 1998-159543/14.  
 DR N-PSDB; AAV20947.  
 XX ACC synthase and ACC oxidase from coffee, Coffea arabica - and  
 PT encoding DNA, useful in methods to control coffee bean ripening e.g.  
 PT to allow synchronous ripening and thus more productive harvesting  
 XX Claim 1; Fig 1; 72pp; English.  
 XX The present sequence is Coffea arabica, coffee-fruit specific  
 CC 1-aminocyclopropane-1-carboxylic acid (ACC) synthase.  
 CC ACC synthase cDNA can be used to control ethylene biosynthesis in  
 CC coffee plants, as ACC synthase is an element of the ethylene  
 CC biosynthesis pathway. Transformation of wild-type coffee plants  
 CC with constructs containing the cDNA in an antisense orientation  
 CC can block ACC synthase synthesis. The cDNA can also be used to  
 CC block ACC synthase synthesis by co-suppression. Plants transformed  
 CC with the cDNA are incapable of synthesising ethylene, which is  
 CC necessary in the final stages of fruit ripening in coffee,  
 CC therefore ethylene application enables fruit ripening to be  
 CC controlled, e.g. application to the entire plant can synchronise  
 CC ripening. Coffee beans are preferably obtained from mature fruit,  
 CC but non-uniform ripening has necessitated laborious hand-picking,  
 CC or low yields and productivity when harvesting by strip harvesting  
 CC or mechanical techniques. The ability to synchronise ripening  
 CC makes mechanical harvesting more productive.  
 XX Sequence 504 AA;  
 SQ

Query Match 69.0%; Score 1765; DB 19; Length 504;  
 Best Local Similarity 65.3%; Pred. No. 6.6e-168;  
 Matches 326; Conservative 83; Mismatches 66; Indels 24; Gaps 5;  
 QY 7 DQTPLLSKMAIGDGHGSSPYFDGKAYDQNPFPHTDNPNGVMQGLAENQLTSDLVEDW 66  
 Db 8 eqqqlskmatndghenspyfdgkaydsdpybptrnpgvigmqlaenqlctdlleew 67  
 QY 67 ILANPEASICTPEGINDFRATANFDYHGLAEFRNAVAKFMRGRNRTFDPDRIVMSG 126  
 Db 68 vlnnpeasictaeganxfmevalyqdyhgipefrnavarmekvrgdrvtfdpnrvmsg 127  
 QY 127 GATGAHEVTAFLADPGEAFVLPIPPYPGFDRDLRWRTGKLVPMVMDSSNNFVLTKEAL 186  
 Db 128 gatgahetlafcladpdafivptpypgfdrlwrtgmlpivcrsndfvtkesm 187  
 QY 187 EDAYEKARENIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCEIYAATVF 246  
 Db 188 eayqkageanirvkfgllnpsnplgtvldretlglvtfndknhlcldeiyatsvf 247  
 QY 247 SQPGFISAEITLEDTECDRLNHLVIVSLSKDMGPPGFRVGIYISYNDVAVNCARKMS 306  
 Db 248 sqpfisiselieh--dvqcnrdihivyslskdgtfpgfrvgyvgyndvavncarkms 305





SQ Sequence 486 AA;

Query Match 68.9%; Score 1762.5; DB 18; Length 486;  
 Best Local Similarity 67.7%; Pred. No. 1:1e-167;  
 Matches 325; Conservative 68; Mismatches 72; Indels 15; Gaps 3;

QY 8 QTPLLSKWAIGDGHGESSPYFDGHWKAYDQNPFFHTDNPNGVMQGLAENQLTSLDVEDWI 67  
 DB 4 qhqlskiatndngenspyfdgwkaydnpfhtdnpdngvigmqlaenqlsadsiidwi 63  
 QY 68 LNPPEASICTPEGINDFRAITANFODYHGLAEFRNAVAFKARTGRNITFDPPDRIVMSGG 127  
 DB 64 kkhpkasincpeghvmfkdlanfqdyhglpefrqaiakfmgrrvgrvtdpdrivmsgg 123  
 QY 128 ATGAHEVTACLDAPGBAFLVPIPIYPYPGFDRDLRWRTGVKLVPVCMDCSSNNFVLTKEALE 187  
 DB 124 atganelimfcladpgdafivpsypafyrdlgwrtgvqivpvcddssnnfqtikvale 183  
 QY 188 DAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDDEIYAATVFS 247  
 DB 184 aaydakagdggnvkgllitnpsnplgtldretlcklslfneknihlvcddeiyaatifs 243  
 QY 248 QPGFISAEILEDETDIECDNLVHIIVYSLSKDMGFFGFRVGIYSYNDVAVNCARKMSS 307  
 DB 244 sqnfavseveleevmd--cndllihivyslskdmglpgfrvgyvsvndavvncgrkms 301  
 QY 308 FGLVSTOTQYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGGLAKVGIKCLQSNAGLFV 367  
 DB 302 fglvssqtqyllasmladeefvdlaseekrlkkrhgtfkglegigiscleskaglfv 361  
 QY 368 WMDLRQLLKPTFDSSETELMKVITHEVKINVSFGYSPCHTEPGWFRVCYANMDDMAVOIA 427  
 DB 362 wmdlrhllkeqtdngemelwrvlndvknvpsgshcvepgwfrvcfanmddetleiva 421  
 QY 428 LQIRNEV-----LQNEVVYSNKKHCWHSNLRSLKTRRDD-----ITMSPHSPL 474  
 DB 422 lkrthafveqkeretistktkdmptskcwkknrlisfsrifeegigspiansphspl 481

RESULT 10  
 ID AAE00985 standard; Protein; 485 AA.  
 AC AAE00985;  
 XX AAE00985;  
 DT 04-JUL-2001 (first entry)  
 XX Tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC 1A.  
 DE Tomato; 1-aminocyclopropane-1-carboxylic acid synthase; LE-ACC 1A;  
 KW ethylene production; fruit ripening; transgenic plant.  
 XX Lycopersicon esculentum.  
 OS US6207881-B1.  
 XX US6207881-B1.  
 XX 27-MAR-2001.  
 XX 25-JAN-1995; 95US-0378313.  
 XX 19-APR-1992; 92US-0862493.  
 PR 10-SEP-1990; 90US-0579896.  
 XX (USDA ) US SEC OF AGRIC.  
 XX Theologis A, Sato T;  
 XX WPI; 2001-289591/30.  
 XX Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic  
 PT acid synthase, LE-ACC2 useful for producing ACC synthase which is  
 PT essential for the production of ethylene in higher plants

XX Example 3; Fig 10; 92pp; English.  
 XX The present sequence is tomato 1-aminocyclopropane-1-carboxylic acid  
 CC synthase, LE-ACC 1A. ACC synthase are capable of catalysing the  
 CC conversion of AdoMet (S-adenosyl methionine) to ACC and methyl  
 CC thioadenosine (MTA). ACC DNA is useful for producing ACC synthase which  
 CC is essential for the production of ethylene in higher plants, where  
 CC ethylene is a determinant of fruit ripening. The ACC DNA is also useful  
 CC for producing transgenic plants which are overproducers of or are  
 CC deficient in ACC synthase.  
 XX Sequence 485 AA;  
 SQ

Query Match 68.6%; Score 1755.5; DB 22; Length 485;  
 Best Local Similarity 68.8%; Pred. No. 5.6e-167;  
 Matches 327; Conservative 76; Mismatches 65; Indels 7; Gaps 5;

QY 11 LLSKMAIGDGHGESSPYFDGHWKAYDQNPFFHTDNPNGVMQGLAENQLTSLDVEDWILNN 70  
 DB 13 llsklatndngenspyfdgwkayannpffhtdnpdngvigmqlaenqlcfdliqewvwnn 72  
 QY 71 PEASICTPEGINDFRAITANFODYHGLAEFRNAVAFKARTGRNITFDPPDRIVMSGGATG 130  
 DB 73 pkasictvegaenfqdiaifqdyhglpefrqavafmekvrgvtdfnpnrvmsggatg 132  
 QY 131 AHEVTACLDAPGBAFLVPIPIYPYPGFDRDLRWRTGVKLVPVCMDCSSNNFVLTKEALEDAY 190  
 DB 133 ahemlafcladpgdafivptpypgfdrdlrwtgvqlfpvvcscndfkvtkaaleay 192  
 QY 191 EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDDEIYAATVFSQPG 250  
 DB 193 ekaggsnikkgllitnpsnplgtldrtdlrdvtfinsknihlvcddeiyaatvfdqpr 252  
 QY 251 FISAEILEDETDIECDNLVHIIVYSLSKDMGFFGFRVGIYSYNDVAVNCARKMSSSGL 310  
 DB 253 fisvseivdm--lecnkdlhivyslskdmglpgfrvgyvsvndvtnlarkmssfgl 310  
 QY 311 VSTOTQYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGGLAKVGIKCLQSNAGLFVMD 370  
 DB 311 vstqthllasmladeefvdlkfaesserlgerqgmftkglaevgistlkanaglfvmd 370  
 QY 371 LRQLLKPTFDSSETELMKVITHEVKINVSFGYSPCHTEPGWFRVCYANMDDMAVOIALQR 430  
 DB 371 lrrllkeatfdelelwrllneknvpsgshcvepgwfrvcfanmddetmtrialkr 430  
 QY 431 IRNEVLQNKVEY--VVSNNKKHCWHSNLRSLKTRRDD-DITMSP-HSPLQSPMVK 481  
 DB 431 isyfvlpqginniaaikkqcsrrklqislsfrldhefmspahspm-nspivr 484

RESULT 11  
 ID AAB59723 standard; Protein; 485 AA.  
 XX AAB59723;  
 AC AAB59723;  
 XX 29-MAR-2001 (first entry)  
 XX Tomato ACC synthase gene LE-ACC1A(b) clone.  
 DE Tomato  
 KW ACC synthase; 1-aminocyclopropane-1-carboxylic acid synthase; enzyme;  
 XX ethylene production; fruit ripening; tomato; LE-ACC.  
 OS Lycopersicon esculentum.  
 XX US6156956-A.  
 XX 05-DEC-2000.  
 PD 02-MAR-1998; 98US-0033349.  
 XX

PR 25-JAN-1995; 95US-0378313.  
PR 02-APR-1992; 92US-0862493.  
PR 07-JUN-1995; 95US-0481171.  
PR 10-SEP-1990; 90US-0579896.  
PA (USDA ) US DEPT OF AGRICULTURE.  
XX Sato T, Theologis A;  
XX WPI; 2001-079558/09.  
XX Expression cassette for producing transgenic plants exhibiting  
PT inhibited ethylene production and delayed fruit ripening, comprises  
PT complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic acid  
PT synthesis  
XX  
XX Example 3; Fig 10; 91pp; English.  
XX  
XX 1-aminocyclopropane-1-carboxylic acid (ACC) synthase is essential for  
CC the production of ethylene in higher plants; ethylene is a determinant  
CC of fruit ripening. The present invention relates to an expression  
CC cassette which comprises the reverse transcript of RNA complementary to  
CC an RNA transcribed from ACC synthase gene. The expression cassette can be  
CC used to prevent ACC gene expression. The expression cassette is useful  
CC for inhibiting ethylene production and fruit ripening, when introduced  
CC into a plant or plant cells. The present sequence is the protein encoded  
CC by tomato ACC synthase gene LE-ACC1A(b) clone. This sequence was used in  
CC a sequence homology comparison with other ACC synthase gene clones  
CC (AAB59721-B59727).  
XX  
XX Sequence 485 AA;  
XX  
Query Match 68.6%; Score 1755.5; DB 22; Length 485;  
Best Local Similarity 68.8%; Pred. No. 5.6e-167;  
Matches 327; Conservative 76; Mismatches 65; Indels 7; Gaps 5;  
QY 11 LLSKMAIGDGHGESSPYFDGWKAYDONPPHPTDNPNGVMQGLAENQLTSDLVEDWILNN 70  
DB 13 llsklatndghgkayannphtldnptgvmqglanqlcfldlqewvnn 72  
QY 71 PRASICTPGINDFRAINFQDHYHGLAEFRNAVAFMARTGNRTTFDPRIVMSGGATG 130  
DB 73 pksactvegaenfdiaifqdyhglpeirgavarfmevrgdrvtfdpnrvmsggatg 132  
QY 131 AHEVTAFLADPGEAFPIPIYPGFDRLRWRTGKLVPMCDSSNNFVLTKEALEDAY 190  
DB 133 ahemlafcladpgdaflvptpgfdrldrtgvtgvlfpvvescndfkvttkaleay 192  
QY 191 EKAREDNIRVKGLLTNPSPNPLGTMDRKTLTVTVSFINEKRIHLVCDIYAATVFSQPG 250  
DB 193 ekaqgnlkikgllnnpsnplgtlldktdlrdvtfnsknhlvcdeiyatvfdqpr 252  
QY 251 FTSIARILEDETDICDRNLHVIVSLSDMGFPFGFRVGIYISNDVAVNCARKMSSFG 310  
DB 253 flsvseivedm--iecnkdlhlvyslsgldgfpgrvgtvysndvtnarkmssfgl 310  
QY 311 VSTQYQYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGLAKRVGKICLQSNAGLFVWMD 370  
DB 311 vstqqtqllasmlsdevfidkfaesserlgerqgmftkgaevgistlksnaglfvwm 370  
QY 431 IRNFVLQKREV--VVSNNKKHNSLRSLKTRRFD-DITMSP-RHSPQSPWVK 481  
DB 431 isyfvlpqglnniaalkqcsrrklqslsfrldhefmsnpsahpm-nsplvr 484  
RESULT 12  
AAR15508  
ID AAR15508 standard; Protein; 485 AA.

XX AAR15508;  
XX 17-DEC-2001 (updated)  
DT 09-MAR-1992 (first entry)  
XX Tomato ACC synthase encoded by clone LE-ACC1A.  
DE 1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening.  
KW Lycopersicon esculentum c.v. Rutgers.  
OS  
XX USN7579896-N.  
XX 12-NOV-1991.  
XX 10-SEP-1990; 90US-0579896.  
XX 10-SEP-1990; 90US-0579896.  
PA (USDA ) US SEC OF AGRICULTURE.  
XX Theologis A, Sato T;  
XX WPI; 1991-368895/50.  
XX DNA encoding ACC synthase - used for control of plant development  
PT and for prodn. of ACC synthase, ethylene and ethanol  
XX  
XX Disclosure; Fig 14; 73pp; English.  
XX  
XX Genomic clone LE-ACC1A was one of four different clones identified  
CC in a library prepared from total DNA extracted from etiolated Rutgers  
CC seedlings. Screening was by the cDNA clone pACC1 (see AAQ15134). The  
CC amino acid sequence was deduced from the cDNA and shows  
CC considerable homology with ACC sequences deduced from the three other  
CC tomato and the zucchini clones.  
CC See AAQ15131-Q15140.  
CC (Note: Revised entry submitted to correct the patent number format of  
CC US Government-owned NTIS applications to prevent clashes with ongoing US  
CC granted patent numbers. For further information please visit the Derwent  
CC web site at [www.derwent.com/dwpi/updates/ntis\\_us.html](http://www.derwent.com/dwpi/updates/ntis_us.html).)  
XX  
XX Sequence 485 AA;  
XX  
Query Match 68.2%; Score 1746.5; DB 12; Length 485;  
Best Local Similarity 68.6%; Pred. No. 4.5e-166;  
Matches 326; Conservative 76; Mismatches 66; Indels 7; Gaps 5;  
QY 11 LLSKMAIGDGHGESSPYFDGWKAYDONPPHPTDNPNGVMQGLAENQLTSDLVEDWILNN 70  
DB 13 llsklatndghgkayannphtldnptgvmqglanqlcfldlqewvnn 72  
QY 71 PRASICTPGINDFRAINFQDHYHGLAEFRNAVAFMARTGNRTTFDPRIVMSGGATG 130  
DB 73 pksactvegaenfdiaifqdyhglpeirgavarfmevrgdrvtfdpnrvmsggatg 132  
QY 131 AHEVTAFLADPGEAFPIPIYPGFDRLRWRTGKLVPMCDSSNNFVLTKEALEDAY 190  
DB 133 ahemlafcladpgdaflvptpgfdrldrtgvtgvlfpvvescndfkvttkaleay 192  
QY 191 EKAREDNIRVKGLLTNPSPNPLGTMDRKTLTVTVSFINEKRIHLVCDIYAATVFSQPG 250  
DB 193 ekaqgnlkikgllnnpsnplgtlldktdlrdvtfnsknhlvcdeiyatvfdqpr 252  
QY 251 FTSIARILEDETDICDRNLHVIVSLSDMGFPFGFRVGIYISNDVAVNCARKMSSFG 310  
DB 253 flsvseivedm--iecnkdlhlvyslsgldgfpgrvgtvysndvtnarkmssfgl 310  
QY 311 VSTQYQYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGLAKRVGKICLQSNAGLFVWMD 370  
DB 311 vstqqtqllasmlsdevfidkfaesserlgerqgmftkgaevgistlksnaglfvwm 370





Job time: 6087 sec

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OM protein - protein search, using sw model

Run on: August 21, 2002, 02:08:55 ; Search time 24.39 Seconds  
(without alignments)  
768.358 Million cell updates/sec

Title: US-09-763-957-2  
Perfect score: 2559  
Sequence: 1 MGFKAMDQPLLSKMAIGDG.....DITMSPHSLPQSPVWKATN 484

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2354	92.0	484	1	1A1C_SOYBN
2	1927	75.3	368	1	1A1C_PHAU
3	1739.5	68.0	491	1	1A1C_TOBAC
4	1713	66.9	485	1	1A12_LYCES
5	1698.5	66.4	492	1	1A11_PROMU
6	1640.5	64.1	493	1	1A11_CUCMA
7	1637.5	64.0	493	1	1A11_CUCPE
8	1627.5	63.6	494	1	1A12_CUCPE
9	1603.5	62.7	517	1	1A1C_DIACA
10	1584	61.9	476	1	1A14_LYCES
11	1578	61.7	496	1	1A12_ARATH
12	1341	52.4	473	1	1A1C_MALDO
13	1339.5	52.3	475	1	1A12_CUCMA
14	1258.5	49.2	487	1	1A11_ORYSA
15	293.5	11.5	394	1	AAT_AQUAE
16	276.5	10.8	392	1	AAT_BACSP
17	274.5	10.7	397	1	AAT_STRVG
18	263	10.3	392	1	PATA_BACSU
19	256.5	10.0	393	1	AAT1_BACSU
20	252	9.8	370	1	AAT2_METJA
21	248.5	9.7	393	1	AAT_BACST
22	248	9.7	377	1	AAT_THEMA
23	229	8.9	412	1	AAT_RICPR
24	227	8.9	389	1	AAT_PYRAB
25	225.5	8.8	410	1	AAB1_RHIME
26	225	8.8	383	1	AAT_THAQ
27	224	8.8	416	1	ATTY_TRYCR
28	222.5	8.7	410	1	AAB2_RHIME
29	220.5	8.6	399	1	AAT2_BACSU
30	220	8.6	482	1	ALA2_PANMI
31	217.5	8.5	482	1	ALA2_HORVU
32	217	8.5	385	1	AAT_THETH
33	216.5	8.5	429	1	AAT_MYCTU

34	216.5	8.5	507	1	ALAT_YEAST
35	213.5	8.3	454	1	ATTY_RAT
36	202.5	7.9	412	1	YFDZ_ECOLI
37	201.5	7.9	495	1	ALAT_HUMAN
38	200	7.8	405	1	YFBO_ECOLI
39	196.5	7.7	404	1	YFBO_HAEN
40	196.5	7.7	454	1	ATTY_HUMAN
41	194.5	7.6	505	1	ALAT_SCHPO
42	194.5	7.6	592	1	ALAM_YEAST
43	194	7.6	391	1	AAT_PYRHO
44	189.5	7.4	389	1	AAT_SYNY3
45	187.5	7.3	375	1	AAT1_METJA

ALIGNMENTS

RESULT 1  
1A1C\_SOYBN STANDARD; PRT; 484 AA.  
AC P31531;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC  
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).  
GN ACS1;  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. CENTURY; TISSUE=Leaf;  
RA Liu D, Li N, Mattoso A, et al.  
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-  
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.  
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine -> L-  
CC aminocyclopropane-1-carboxylate + methylthioadenosine.  
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.  
CC -!- SUBUNIT: HOMODIMER.  
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
CC AMINOTRANSFERASES.  
CC -----  
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CC -----  
CC EMBL; X67100; CAA47474.1;  
CC PIR; S25002; S25002.  
CC HSP; P37821; 1B8G.  
CC Mendel; 8361; GLYMa; Acs;1.  
CC InterPro; IPR001176; ACC-synthase.  
CC Pfam; PF00155; aminotran\_1.2; 1.  
CC InterPro; IPR001511; ACCsynthase.  
CC PRINTS; PR00753; ACCSYNTHASE.  
CC PROSITE; PS00105; AA-TRANSFER CLASS.1; 1.  
CC Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;  
CC Multigene family. 279 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
FT BINDING 279  
SQ SEQUENCE 484 AA; 54730 MW; 152E7AD12B992987 CRC64;

Query Match 92.0%; Score 2354; DB 1; Length 484;  
Best Local Similarity 90.9%; Pred. No. 4.5e-174;  
Matches 439; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

QY 1 MGKAMQDTPLLSKMAIGDHGESSPYFDGNKAYDQNFPHFTDNPNGVMQGLAENQULTS 60  
DB 1 MGLMDVDQTLSSKMAIGDHGESSPYFDGNKAYDQNFPHFTDNPNGVMQGLAENQULTS 60  
QY 61 DLVEDWILNNPEASICTPEGINDFRAIANFQDYGHLAEFRNAVAKFMAKRNITFDPPD 120  
DB 61 DLVEDWILNNPEASICTPEGINDFRAIANFQDYGHLAEFRNAVAKFMAKRNITFDPPD 120  
QY 121 RIVMSGGATGAHEVTAFCADPGGAFLVPIYPYCGFDRLRWRTGKLVPMVCMSSNNFV 180  
DB 121 RIVMSGGATGAHEVTAFCADPGGAFLVPIYPYCGFDRLRWRTGKLVPMVCMSSNNFV 180  
QY 181 LTKALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFNEKRIHLVCDDEI 240  
DB 181 LTKALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFNEKRIHLVCDDEI 240  
QY 241 YAATVFSQPGFTSIAEILEDTECDRLNHLVHIVYSLSKDGMFGFRGVCIISYNDVAVN 300  
DB 241 VSATVFSHPSTISIAEILEDTECDRLNHLVHIVYSLSKDGMFGFRGVCIISYNDVAVN 300  
QY 301 CARMKSSFGVSTQYLLASMLNDEFEVERFLAESAKRLAQRFVFTGGGLAKVGKICLQ 360  
DB 301 CARMKSSFGVSTQYLLASMLNDEFEVERFLAESAKRLAQRFVFTGGGLAKVGKICLQ 360  
QY 361 SNAGLFVWMDLRQLLKKPTFSETELKVIHIVKINSPGYSFHCFTGPGFVRCYANMD 420  
DB 361 SNAGLFVWMDLRQLLKKPTFSETELKVIHIVKINSPGYSFHCFTGPGFVRCYANMD 420  
QY 421 DMVAQIALQIRINFLQNKVNVKNCWHSNLSLKTREDDITWSPHPLQSPMV 480  
DB 421 DMVAQIALQIRINFLQNKVNVKNCWHSNLSLKTREDDITWSPHPLQSPMV 480  
QY 481 KAT 483  
DB 481 KAT 483

RESULT 2  
ID 1A1C PHAAU STANDARD; PRT; 368 AA.  
AC Q01912;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC  
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase)  
DE (Fragment).  
CN ACS5.  
OS Phaseolus aureus (Mung bean) (Vigna radiata).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
OX NCBI\_TaxID=3916;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. BERKEN / RWILC2; TISSUE=Hypocotyl;  
RX MEDLINE=93043033; Pubmed=1421146;  
RA Botella J.R., Arteca J.M., Schlaghauer C.D., Arteca R.N.,  
RA Phillips A.T.;  
RT "Identification and characterization of a full-length cDNA encoding  
RT for an auxin-induced 1-aminocyclopropane-1-carboxylate synthase from  
RT etiolated mung bean hypocotyl segments and expression of its mRNA in  
RT response to indole-3-acetic acid.";  
RL Plant Mol. Biol. 20:425-436(1992).  
CC 1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-  
CC CARBOXYLATE. A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.  
CC 1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 1-  
CC aminocyclopropane-1-carboxylate + methylthioadenosine.  
CC 1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC 1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.  
CC 1- SURUNIT: HOMODIMER.  
CC 1- INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS

CC MECHANICAL WOUNDING AND A NUMBER OF CHEMICALS.  
CC 1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
CC AMINOTRANSFERASES.  
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CC -----  
CC EMBL; Z11562; CAA77655.1; -  
DR HSSP; P37821; 188G.  
DR Mendel; 9876; PHAAU; Acs; 5.  
DR InterPro; IPR001511; Aminotran\_1.  
DR Pfam; PF001155; aminotran\_1.2; 1.  
DR PROSITE; PS00105; AA-TRANSFER-CLASS\_1; 1.  
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;  
KW Multigene family.  
FT NON\_TER 1  
FT BINDING 230 230  
FT NON\_TER 368 368  
FT NON\_TER 368 368  
SQ SEQUENCE 368 AA; 41477 MW; 31BA61D5FC2DACB8 CRC64;  
Query Match 75.3%; Score 1927; DB 1; Length 368;  
Best Local Similarity 99.7%; Pred. No. 2.6e-141;  
Matches 367; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 50 QMGLAENQLTSLVEDWILNNPEASICTPEGINDFRAIANFQDYGHLAEFRNAVAKFMAKRNITFDPPD 109  
DB 1 QMGLAENQLTSLVEDWILNNPEASICTPEGINDFRAIANFQDYGHLAEFRNAVAKFMAKRNITFDPPD 109  
QY 110 TRGNRITFDPPDRIVMSGGATGAHEVTAFCADPGGAFLVPIYPYCGFDRLRWRTGKLV 169  
DB 61 TRGNRITFDPPDRIVMSGGATGAHEVTAFCADPGGAFLVPIYPYCGFDRLRWRTGKLV 120  
QY 170 PYMCDSSNNFVLTKEALDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFTN 229  
DB 121 PYMCDSSNNFVLTKEALDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFTN 180  
QY 230 EKRIHLVCDDEIYAATVFSQPGFTSIAEILEDTECDRLNHLVHIVYSLSKDGMFGFRGV 289  
DB 181 EKRIHLVCDDEIYAATVFSQPGFTSIAEILEDTECDRLNHLVHIVYSLSKDGMFGFRGV 240  
QY 290 IYISYNDVAVNCARKMSFGLVSTQYLLASMLNDEFEVERFLAESAKRLAQRFVFTG 349  
DB 241 IYISYNDVAVNCARKMSFGLVSTQYLLASMLNDEFEVERFLAESAKRLAQRFVFTG 300  
QY 350 GLAKVGKICLQSNAGLFVWMDLRQLLKKPTFSETELKVIHIVKINSPGYSFHCFTG 409  
DB 301 GLAKVGKICLQSNAGLFVWMDLRQLLKKPTFSETELKVIHIVKINSPGYSFHCFTG 360  
QY 410 GWFRCVYA 417  
DB 361 GWFRCVYA 368  
RESULT 3  
ID 1A1C\_TOBAC STANDARD; PRT; 491 AA.  
AC Q07262;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC  
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).  
GN ACSL.  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.



```
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. XANTHI;
RA Bailey B.A., Avni A., Li N., Matoo A.K., Anderson J.D.;
RT "Nucleotide sequence of the Nicotiana tabacum cv Xanthi gene encoding
RL Plant Physiol. 100:1615-1616(1992).
CC -!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; X65982; CAA46797.1; -.
DR HSSP; P37821; 1B8G.
DR Mendel; 252; NICta; Accs;1.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran.1.
DR Pfam; PF00155; aminotran.1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate.
KW BINDING 278 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT SEQUENCE 491 AA; 55290 MW; 57B9FF4306686DFD CRC64;
SQ
Query Match 68.0%; Score 1739.5; DB 1; Length 491;
Best Local Similarity 66.5%; Pred. No. 1.1e-126;
Matches 326; Conservative 71; Mismatches 84; Indels 9; Gaps 5;
QY 1 MGFANDQTPLLSKMAIGDGHGESSYFDGKAYDQNPHTDNPNGVMQGLAENQLTS 60
DB 1 MGFENEKNSILSKLATNEELGENSEPYFDGKAYDNDPFLPNKPNGVQMGLEAENQLCF 60
QY 61 DLVEDILNPEASICTPEGINDFRAINFQDYHGLAEFRNAVAKEMARTGRNRTFDPD 120
DB 61 DLIEWIKRNPASICTTEGKSFRAINFQDYHGLPEFRSAKAKEMKTRGGRVTFDPE 120
QY 121 RYVMSGGATGAHEVTAFCADPGAEFLVPIYPYDFDRDLRWRTGTVKLVPMCDSSNNFV 180
DB 121 RYVMAGGATGANETIIFCLADTGDALVSPYPYPAFNRLRLRWRTGVQLPIPCDSSNNFQ 180
QY 181 LKFEALDAYEKAREDIRVKGILLINPSNPLGTIMDRKTLRTVSVFNEKRLHLCVDEI 240
DB 181 ITTKAYREAYEAKNSKIKVGLILNPSNPLGTTDLDTLKNLLFTFOHNLHLCVDEI 240
QY 241 YAATVFSQPFISIAILEDTEIDCDRLNHLVIVISLXDMGPPGFRVGIYSYNDAVYN 300
DB 241 YAATVNTQFVSIAILIDDETS-HCNKDLVHLVIVISLXDMGLPGRVGLVYSFNDAVYN 299
QY 301 CARKMSFGLVSTQTOYLLASMLNDDFEVFRFLAESAKRLAQRFRVFTGSLAKVIGKCLQ 360
DB 300 CARKMSFGLVSTQTOYLLAEMLSDERFSNFTLESSKRLAKRKHFTNGLEEVGKCLR 359
QY 361 SNAGLFWMDLRLKLPKTFDSTELWKYIIIEVKLVNSPGYFHCTEPGWFRVCANMD 420
DB 360 SNAGLFCWMDLRLPKKSTFDSMSLWRVIINDVKLVNSPGSSFDQCEPGFRVCANMD 419
QY 421 DMAVQIALQIRNFVLQNE-----VVVSNKKHCW-HSNLRLSLKTRRDPD-ITMSP-HS 472
DB 421 DMAVQIALQIRNFVLQNE-----VVVSNKKHCW-HSNLRLSLKTRRDPD-ITMSP-HS 472
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Db 420 DETVDIALAIRSFVGVKKSGDESTPILMEKKQOWKKNLRLSFSKRMYSYNLSPSS 479

QY 473 PLPQSPMWKA 482  
|:| |:|:|

Db 480 PIPHSPLVRA 489

RESULT 4

IA12\_LYCES STANDARD; PRT; 485 AA.

AC P18485;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 1-aminocyclopropane-1-carboxylate synthase 2 (EC 4.4.1.14) (ACC synthase 2) (S-adenosyl-L-methionine methylthioadenosine-lyase 2) (ACS-2).

DE (ACS-2).

GN ACS2 OR ACC2 OR PCW4A.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Embryophyta; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OX NCBI\_TaxID=4081;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Etolated hypocotyl;

RX MEDLINE=92106351; PubMed=1762159;

RA Rottmann W.H., Peter G.F., Oeller P.W., Keller J.A., Shen N.F., Nagy B.P., Taylor L.P., Campbell A.D., Theologis A.;

RT "1-aminocyclopropane-1-carboxylate synthase in tomato is encoded by a multigene family whose transcription is induced during fruit and floral senescence.";

RT J. Mol. Biol. 222:937-961(1991).

RN [2]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=CV. ORLANDO; TISSUE=Fruit;

RX MEDLINE=90280476; PubMed=2191304;

RA van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

RT "Cloning and sequence of two different cDNAs encoding 1-aminocyclopropane-1-carboxylate synthase in tomato.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:4859-4863(1990).

CC -!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.

CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-aminocyclopropane-1-carboxylate + methylthioadenosine.

CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.

CC -!- SUBUNIT: HOMODIMER.

CC -!- INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS MECHANICAL WOUNDING AND A NUMBER OF CHEMICALS.

CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.

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CC -----

DR EMBL; X59139; CAA41855.1; -.  
DR EMBL; X59145; CAA41856.1; -.  
DR EMBL; M34289; AAA81580.1; -.  
DR PIR; S19677; S19677.  
DR PIR; S19678; S19678.  
DR PIR; A35516; A35516.  
DR HSSP; P37821; 1B8G.  
DR Mendel; 509; LYCES; Accs;2.  
DR InterPro; IPR001176; ACC\_synthase.  
DR InterPro; IPR001511; Aminotran.1.  
DR Pfam; PF00155; aminotran.1.2; 1.  
DR PRINTS; PR00753; ACCSYNTHASE.

DR PROSITE; PS00105; AA-TRANSFER\_CLASS\_1; 1.  
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;  
Multigene family.  
FT BINDING 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
FT CONFLICT 124 A -> V (IN REF. 1; CAA41856).  
FT CONFLICT 322 L -> P (IN REF. 2).  
FT CONFLICT 399 P -> L (IN REF. 2).  
SQ SEQUENCE 485 AA; 54662 MW; 40B3F55B5EF0D9C7 CRC64;

Query Match 66.9%; Score 1713; DB 1; Length 485;  
Best Local Similarity 65.6%; Pred. No. 1.2e-124;  
Matches 319; Conservative 72; Mismatches 89; Indels 6; Gaps 4;

QY 1 MGFKAMDQTPLLSKMAIGDHGESSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTS 60  
DB 1 MGFETAKTNSILSKLATNEEHCEHSPYFDGWKAYDSDPFPHPLKPNFVQMGLAENQLCL 60

QY 61 DLVDEWILNPPASCTCTEGINDFRAIANFQDYGHLAEFRNAVAFMARTGRNRTTFDDP 120  
DB 61 DLIEDWIKRNKPGSICS-EGIKSFKAIAFQDYGHLPEFRKAIAKMEKTRGGRVRFDP 119

QY 121 RIVMSGGATGAHEVTAFCADLADGEAFPIPIYPYPGFDRDLRWRGKLVPMCDSSNNFV 180  
DB 120 RYVAGGATGANETIIFCLADPGDAFLVPSPIYPFAPNDRDLRWRGKLVPMCDSSNNFV 179

QY 181 LKAEADAYEKAREDNIRVKGLLITNPSNPLGTIMDKRTLRTVVSFNEKRIHLVCD 240  
DB 180 ITS KAVKAYENAKNSIKVKGLITNPSNPLGTITLTKSLVSTNQHNIHLVCD 239

QY 241 YAATVSPQGFISIAEILEDDETDICDRNLVHIYVSLSKDMGFGPFRVGIYSDAVVN 300  
DB 240 YAATVDFDPPQFVSI AEILDEQEMTYCNKDLVHIYVSLSKDMGLPGFRVGIYSFNDVYN 299

QY 301 CARKMSSFGLVSTQYLLASMLNDEFEVERFLASAKRLAORFVFTGGGLAKVGKICLQ 360  
DB 300 CARKMSSFGLVSTQYFLAAMLSDEKFDVDFLRESARMLGRKHFTNGLEVGIKCLK 359

QY 361 SNAGLFVWMDLRLQKLPFTFSETELWKVYIHEVKINVSFGYSPFCHTBPGRVFCYANND 420  
DB 360 NNAGLFCWMDLRLRESTFSEMSLVRVINDVKLVNPSGSSFCBPGRVFCYANND 419

QY 421 DNAYOIALQIRNFVQLQNEVVVSN---KKHCW-HSNLRSLSKTRFDDITMSP-HSPLP 475  
DB 420 DGTVDIALARIRNFVGVSEKSGDKSSMEKKQWKKNNLRSLSKTRFDDITMSP-HSPLP 479

QY 476 QSPMYK 481  
DB 480 PSPLVR 485

RESULT 5  
1A11\_PRUMU STANDARD; PRT; 492 AA.  
AC 09MB95;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DE 01-MAR-2002 (Rel. 41, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase 1 (EC 4.4.1.14) (ACC  
synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).  
GN ACSL  
OS Prunus mume (Japanese flowering apricot).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Rosales; Rosaceae; Prunus.  
OX NCBI\_TaxID-102107;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mita S., Kirita C., Kato M., Hyodo H.;  
RT "Expression of ACC synthase is enhanced earlier than that of ACC  
oxidase during fruit ripening of mume (Prunus mume).";  
RL Physiol. Plantarum 107:319-328(1999).  
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-

CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.  
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine - 1-  
aminocyclopropane-1-carboxylate + methylthioadenosine.  
CC -1- Cofactor: PYRIDOXAL PHOSPHATE.  
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
AMINOTRANSFERASES.  
CC -----  
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CC -----  
DR EMBL; AB031026; BAA05049.1; -;  
DR InterPro; IPR001176; ACC\_synthase.  
DR InterPro; IPR001511; Aminotran\_1.  
DR Pfam; PF00155; aminotran\_1.2; 1.  
DR PRINTS; PR00753; ACCSYNTHASE.  
DR PROSITE; PS00105; AA-TRANSFER\_CLASS\_1; 1.  
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;  
Multigene family.  
FT BINDING 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
SQ SEQUENCE 492 AA; 55066 MW; 2002047AF2B43D89 CRC64;

Query Match 66.4%; Score 1698.5; DB 1; Length 492;  
Best Local Similarity 66.6%; Pred. No. 1.6e-123;  
Matches 321; Conservative 62; Mismatches 86; Indels 13; Gaps 4;

QY 11 LLSKMAIGDHGESSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTSDFDIEDWILNN 70  
DB 12 LLSKATSEGHGENSPYFDGWKAYDRNPFHTKNGEVQMGLAENQLSDFDIEDWIKKN 71

QY 71 PEASCTPEGINDFRAIANFQDYGHLAEFRNAVAFMARTGRNRTTFDPRVMSGGATG 130  
DB 72 PRASICTPEGVEEFKNVAFIQDYHGFEPFRKAVAFMSKARGRTVFDPRVMSGGATG 131

QY 131 AHEVTAFCADLADGEAFPIPIYPYPGFDRDLRWRGKLVPMCDSSNNFVLTKEALD 190  
DB 132 ANELVMFCADLADGEAFVPSPIYPFAPFDRDLGWRGKLVPMCDSSNNFVLTKEAL 191

QY 191 EKAREDNIRVKGLLITNPSNPLGTIMDKRTLRTVVSFNEKRIHLVCDIYAATVFSOPG 250  
DB 192 EKAQNNINVKGLIITNPSNPLGTITLDRNTLESVEFFNQKNIHLVCDIYAATVFSPT 251

QY 251 FTISAEILEDDETDICDRNLVHIYVSLSKDMGFGPFRVGIYSDAVVNCARKMSSFL 310  
DB 252 FTCSIEVIQ---NMNCPNLIHIVYSLSKDMGLPGLRVGIVSYNDVNVNICKMSSFL 308

QY 311 VSTOYTOYLLASMLNDEFEVERFLASAKRLAORFVFTGGGLAKVGKICLOSAGLVWMD 370  
DB 309 VSSQTHMLPSMLLDEEFVAREFTSPKRLAKRHGFTKGLVEEVINGCLSKAGLVWMD 368

QY 371 LRQLLKPTFSETELWKVYIHEVKINVSFGYSPFCHTBPGRVFCYANNDNAVOIALQ 430  
DB 369 LRRLLDQTFDGEVLMRVINVEVGNVSPGSSFCVCEGFRVFCYANNDDETLEVALR 428

QY 431 TRNFVLQNK----EVVSNKKHCWHSNLRSL---KTRRFDDIT---MSPHSPPLQSPMV 480  
DB 429 INTFVROGKAQDQVQVVKSPKRWKSNLRSLSPSSSTRFRDQESVNVLSPHMSPHSP 488

QY 481 KA 482  
DB 489 RA 490

RESULT 6  
1A11\_CUCMA STANDARD; PRT; 493 AA.  
ID 1A11\_CUCMA

```

AC P23599;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase CWM33 (EC 4.4.1.14) (ACC
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACS1 OR ACCW.
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3661;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakajima N., Mori H., Yamazaki K., Imaseki H.;
RT "Molecular cloning and sequence of a complementary DNA encoding 1-
RT aminocyclopropane-1-carboxylate synthase induced by tissue wounding.";
RL Plant Cell Physiol. 31:1021-1029(1990).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- INDUCTION: BY TISSUE WOUNDING.
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D01032; BAA00838.1; -
DR PIR; JQ0926; JQ0926.
DR HSP; P37821; 188G.
DR Mendl; 244; CUCma; Accs;1.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran.1.
DR Pfam; PF00155; aminotran.1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 279 279 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 493 AA; 55895 MW; F39234AC99CBEF6B CRC64;

Query Match 64.1%; Score 1640.5; DB 1; Length 493;
Best Local Similarity 63.2%; Pred. No. 4.8e-119;
Matches 313; Conservative 74; Mismatches 95; Indels 13; Gaps 6;

QY 1 MGFAMQD--TPLLSKAIGDGHGESSPYFDGKAYDQNFPHPTDNPNGVMQGLAENQL 58
DB 1 MEFHQIDERNQALLSKIAVDGHGESSPYFDGKAYDNDPFPHPEDNPLGVQMGLEAENQL 60
QY 59 TSLDVEDWILNPEASICTPEGINDFRAINFQDYGHLAEFRNAVAKFMARTGRNRTED 118
DB 61 SFDWIDWIKRHPASICTPGLERFASIANFQDYGHLGPEFRNGIASFMGKVRGRVQFD 120
QY 119 PDRIVMSGGATGAHEVTAFLADPGEAFVPIPIYPGDFDRDLRWRTGKVLVPMDCSSNN 178
DB 121 PSRIVMSGGATGASSETVIFCLADPGDAFLVPSYAAFDRLKWRTRAQIRVHCNSSNN 180
QY 179 FVLTKALEADAYEKAREDNTRVGLLITNPSNPLGTTMDRKTITVTVVSFNEKRHLVCD 238
DB 181 FQVTKAALEATYKKAQEAANTKVRGVITNPSNPLGTTMDRKTITVTVFVQNDHILICD 240
QY 239 EIVAATVFSQPGFISIAIELEDIEDICDNLVHIVYSLSKDNGFPFRVGIISYNDV 298

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DB 241 EIVSATVFKAPTFTISIAQIVEEMF--HCKELIHILYSLSKDMLPGFRVGIISYNDV 298
QY 299 VNCARKMSSFGCLVSTQTYLIASMLNDDFEVFERFLASAKRLAQRFRVFTGGLAKVGTC 358
DB 299 VRRARQMSFGCLVSSQTOHLLAAMLSDDEDVDFKFLAENSKRLAERHARFTKELDKMGTIC 358
QY 359 LOSNAGLVFVMDLRQLLKKPTFDSETELMKVVIIEVINSPGYSFHCTEGPWRVCYAN 418
DB 359 LNSNAGVFVMDLRRLKDKDTFAEMELWRVVIINEVKLNVSPGSSFHVTEPGWRVCYAN 418
QY 419 MDDMAVOIALQIRNEV--LQNK---VVSNNKKHCHWSNLR--SLKTRFED--ITMS 469
DB 419 MDDNTVDVALNRHISFVENIDKEDNTVAMPKTRRRNKLRSFSFGRRYDEGNVLNS 478
QY 470 PHSPLQSPVMKATN 484
DB 479 PHTMSPHSPVLIAKN 493

RESULT 7
ID IALL_CUCPE STANDARD; PRT; 493 AA.
AC P23279;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase 1 (EC 4.4.1.14) (ACC
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACC1A.
OS Cucurbita pepo (Vegetable marrow) (Summer squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3663;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-91139670; PubMed-1995630;
RA Sato T., Oeller P.W., Theologis A.;
RT "The 1-aminocyclopropane-1-carboxylate synthase of Cucurbita.
RT Purification, properties, expression in Escherichia coli, and primary
RT structure determination by DNA sequence analysis.";
RL J. Biol. Chem. 266:3752-3759(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91334397; PubMed-1871117;
RA Huang P.-L., Parks J.E., Rottman W.H., Theologis A.;
RT "Two genes encoding 1-aminocyclopropane-1-carboxylate synthase in
RT zucchini (Cucurbita pepo) are clustered and similar but
RT differentially regulated.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7021-7025(1991).
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- INDUCTION: BY WOUNDING IN FRUIT AND ETIOLATED HYPOCOTYLS. BY
CC INDOLEACETIC ACID (IAA)/BENYLADENINE/LICL ONLY IN FRUIT TISSUE.
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; M58323; AAA33113.1; -
DR EMBL; M61195; AAA33111.1; -

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DR PIR: A38649; A38649.
DR HSP: A41141; A41141.
DR HSP: P37821; 1B8G.
DR InterPro: IPR001176; ACC_synthase.
DR Pfam: PF00155; aminotran_1.2; 1.
DR PRINTS: PR00753; ACCSYNTHASE.
DR PROSITE: PS00105; AA-TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 279 279 PYRIDOXAL PHOSPHATE.
FT CONFLICT 177 177 G -> R (IN REF. 2).
SQ SEQUENCE 493 AA; 55779 MW; 921DC3DFB17A6769 CRC64;

Query Match 64.0%; Score 1637.5; DB 1; Length 493;
Best Local Similarity 63.0%; Pred. No. 8.1e-119;
Matches 312; Conservative 74; Mismatches 96; Indels 13; Gaps 6;

QY 1 MGFKAMDQ--TPLLSKMATGDGSGSSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQL 58
Db 1 MGFHQIDERNQALLSKIALDDGHSNPSYFDGWKAYDNDPFPHPENNPLGVQMGLAENQL 60
QY 59 TSDLVEDWILNPEASICTPEGINDFRATANFDYHGLAEFRNAVAKFARTGRNRTFD 118
Db 61 SFDMIVDWIRKHPKPEASICTPEGLERFKSIANFDYHGLPEFRNAVANFMKVRGGRVKFD 120
QY 119 PDRIVMSGGATGAHEVTAFLADPGAEFLVPIYPYPGFDRDLRWRTGVKLVPMVCDSSNN 178
Db 121 PSRIVMSGGATGASETVIFCLADPGDAFLVPSYAGFDRDLKWRTRAQIIRVHCNCSNN 180
QY 179 FVLTKEALDEAYEKAREDNIRVKGLLITNPSNPLGTINDRKTLRTVVSFINKEKRIHLVCD 238
Db 181 FQVTKAALEIAYKKAQENKMKVGIITNPSNPLGTITTDYDRDLTKLTVFVNGHDIHLICD 240
QY 239 EYIAATVFSQPGFISATIELEDETIEDCDNLVHLVYLSKDMGPGFRVGLIYSNDVAV 298
Db 241 EYISATVFKAPTFTSAEIVEQME--HCKKELIHILYLSKDMGLPGFRVGLIYSNDVV 298
QY 299 VNCARKMSFGLVSTQTYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGGLAKVGIKC 358
Db 299 VRRARQMSFGLVSSQTHLAAMLSDDEVDKFLAENSKRVRGERHARTKELDKMGITC 358
QY 359 LOSNAGLFWMDRLRLKDKQTFKAEMELWRVINEVKLVNPSGSSFHVTEPGWFRVCYAN 418
Db 419 MDDMAVOIALQIRNFV--LQNK-----VVVSNKKHCWHSNLR--SLKTRRFD--ITMS 469
Db 419 MDDNTVDVALNIHSFVENIDKEDNTVAMPSKTRHRDNKRLSFSFGRRYDEGNVLNS 478
QY 470 PHSPLPQSPMVKATN 484
Db 479 PHTMSPHSLVIAKN 493

RESULT 8
1A12_CUCPE
ID 1A12_CUCPE STANDARD; PRT; 494 AA.
AC Q00379;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase 2 (EC 4.4.1.14) (ACC
DE synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
GN ACS2 OR ACCLB.
OS Cucurbita pepo (Vegetable marrow) (Summer squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3663;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE-91334397; PubMed-1871117;
RA Huang P., Parks J.E., Rottman W.H., Theologis A.;
RT "Two genes encoding 1-aminocyclopropane-1-carboxylate synthase in
RT zucchini (Cucurbita pepo) are clustered and similar but
RT differentially regulated.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7021-7025(1991).
CC -!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS
CC MECHANICAL WOUNDING AND A NUMBER OF CHEMICALS.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
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-----
DR EMBL; M61195; AAA33112.1; -.
DR PIR; B41141; B41141.
DR HSP; P37821; 1B8G.
DR Mendel; 247; CUCpe;Acs;2.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA-TRANSFER_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 279 279 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 345 345 A -> AS (IN REF. 1; AAA33112).
SQ SEQUENCE 494 AA; 55922 MW; 02AE029AA4912C36 CRC64;

Query Match 63.6%; Score 1627.5; DB 1; Length 494;
Best Local Similarity 63.1%; Pred. No. 4.8e-118;
Matches 311; Conservative 73; Mismatches 96; Indels 13; Gaps 6;

QY 1 MGFKAMDQ--TPLLSKMATGDGSGSSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQL 58
Db 1 MGFHQIDERNQALLSKIALDDGHSNPSYFDGWKAYDNDPFPHPENNPLGVQMGLAENQL 60
QY 59 TSDLVEDWILNPEASICTPEGINDFRATANFDYHGLAEFRNAVAKFARTGRNRTFD 118
Db 61 SFDMIVDWIRKHPKPEASICTPEGLERFKSIANFDYHGLPEFRNAVANFMKVRGGRVKFD 120
QY 119 PDRIVMSGGATGAHEVTAFLADPGAEFLVPIYPYPGFDRDLRWRTGVKLVPMVCDSSNN 178
Db 121 PSRIVMSGGATGASETVIFCLADPGDAFLVPSYAGFDRDLKWRTRAQIIPVHCNCSNN 180
QY 179 FVLTKEALDEAYEKAREDNIRVKGLLITNPSNPLGTINDRKTLRTVVSFINKEKRIHLVCD 238
Db 181 FQVTKAALEIAYKKAQENKMKVGIITNPSNPLGTITTDYDRDLTKLTVFVNGHDIHLICD 240
QY 239 EYIAATVFSQPGFISATIELEDETIEDCDNLVHLVYLSKDMGPGFRVGLIYSNDVAV 298
Db 241 EYISATVFKAPTFTSAEIVEQME--HCKKELIHILYLSKDMGLPGFRVGLIYSNDVV 298
QY 299 VNCARKMSFGLVSTQTYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGGLAKVGIKC 358
Db 299 VRRARQMSFGLVSSQTHLAAMLSDDEVDKFLAENSKRVLGERHARTKELDKMGITC 358
QY 359 LOSNAGLFWMDRLRLKDKQTFKAEMELWRVINEVKLVNPSGSSFHVTEPGWFRVCYAN 418
Db 359 LNSNAGVFWMDRLRLKDKQTFKAEMELWRVINEVKLVNPSGSSFHVTEPGWFRVCYAN 418
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Query Match      62.7%   Score 1603.5; DB 1; Length 517;
Best Local Similarity 58.5%; Pred. No. 3.6e-116;
Matches 303; Conservative .80; Mismatches 96; Indels 39; Gaps 5;

Qy      1 MG-FKAMDQPTLLSKMIGDGHGSSPYFDGWKKAYDONPFHTDPNGVMQMGLAENOLT 59
|| :| : ||||| :||||| :||||| :||| :||| :||| :||| :||| :||| :||| :|||
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Db 1 MGSYGVYDREILISKIATNDGHNLEYLEYEDGWKAYDRDPYHSTKNSNGVQIOMGLAENOLC 60

Qy 60 SDLVEDILANNPASICTPEGINDFRAIENFODYHGLAEFRNAVAKFMARTGRNITFDP 119

Db 61 FDLVTEWLLANPQASICTNSGVKNKPMWIAIFQDYHGLPEFRSAVAKFMKGARDEKVIENP 120

Qy 120 DRIVMSGGATGAHEVTAFCIADPGEAPLVPDPYYPGDFDRDLKWRGVKLVPMVCDSSNNF 179

Db 121 DRIVMSGGAS-ASETLLFLCLANPGDAFLIPSPYPYPAFNDRDLRWRTGVNLIPTCSSNNF 179

Qy 180 VLNKEALEDAYEKARENDIRVKGCLLLTNPSNPLGTTMDRKTTLTVVSTFNEXRIHLVCD 239

Db 180 KITKEAQAAYEDDALKNHKIKVGIITNPSNPLGTVLDKDTLKMULLTFVNAKNIHLVCD 239

Qy 240 IYAATVSPQCFISIAEILEDIEDIRNLVHIVYSLSKDMGFGFCFRGVIISYNDVAV 299

Db 240 IYATTVNSPFSFISVAEVIKDPHV--NODLVHILYSLSKDMGFGFCFRGVIISYNDRV 297

Qy 300 NCARKMSFGLVSTQYQLLASMLNDEFVRFLEASAKRLAQRVFTVGGGLAKVIGIKCL 359

Db 298 STARRMSFGLVSSQTFMIAALLSDDDFVRRLFLVESRDRLFRHQHFTSELAKIGICGL 357

Qy 360 QSNAGLEFVMDLRHLLKKPFDSETELWKVITHEVKINVSFGYSFCHTSPGHFRVCYANM 419

Db 358 QGNAALFVMDLRHLLDEATVERELKLRVINEVKINVSPOSSFLCSEPGFWRCVFANM 417

Qy 420 DDMAVQIALQIRNFIQLNK-----EVTYSNKKHCWH 451

Db 418 DNATLDVALNIRSFVTRGVNDSTWTTTSARAATTTTTTTTTTTTTTTTTTTTTTKKRCQ 477

Qy 452 SNLRSLKTRRFD-----ITMSPHSPLQSPMYKA 482

Db 478 MELRSPNNRRFEDGLMSPHSILLSPSPMPQSLVKA 515

RESULT 10

1A14\_LYCES

AC ID 1A14\_LYCES STANDARD; PRT; 476 AA.

AC P29535;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE 1-aminocyclopropane-1-carboxylate synthase 4 (EC 4.4.1.14) (ACC

DE synthase 4) (S-adenosyl-L-methionine methylthioadenosine-lyase 4)

DE (ACS-4).

GN ACS4 OR PCVV4B.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

OC NCBI\_TaxID=4081;

RP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. CARUSO; TISSUE=Etiolated hypocotyl;

RX MEDLINE=93374928; PubMed=8366090;

RA Lincoln J.E., Campbell A.D., Oetiker J., Rottmann W.H., Oeller P.W.,

RA Shen N.F., Theologis A.;

RA "LE-ACS4, a fruit ripening and wound-induced 1-aminocyclopropane-1-

FT carboxylate synthase gene of tomato (Lycopersicon esculentum).

FT Expression in Escherichia coli, structural characterization,

FT expression characteristics, and phylogenetic analysis.";

FT J. Biol. Chem. 268:19422-19430(1993).

RL [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Etiolated hypocotyl;

RX MEDLINE=92106351; PubMed=1762159;

RA Rottmann W.H., Peter G.F., Oeller P.W., Keller J.A., Shen N.F.,

RA Nagy B.P., Taylor L.P., Campbell A.D., Theologis A.;

RT "1-aminocyclopropane-1-carboxylate synthase in tomato is encoded by a

FT multigene family whose transcription is induced during fruit and

FT floral senescence.";

RL J. Mol. Biol. 222:937-961(1991)

RP [3]

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RP SEQUENCE FROM N.A.
RX MEDLINE=91271385; PubMed=1711229;
RA Olson D.C., White J.A., Edelman L., Harkins R.N., Kende H.;
RT "Differential expression of two genes for L-aminocyclopropane-1-
RL carboxylate synthase in tomato fruits.";
RN Proc. Natl. Acad. Sci. U.S.A. 88:5340-5344(1991).

[4]
RP SEQUENCE OF 20-159 FROM N.A.
RC STRAIN=CV. ORLANDO; TISSUE=Fruit;
RX MEDLINE=90280476; PubMed=2191304;
RA van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;
RT "Cloning and sequence of two different cDNAs encoding 1-
RL aminocyclopropane-1-carboxylate synthase in tomato.";
RC Proc. Natl. Acad. Sci. U.S.A. 87:4859-4863(1990).
CC -!- FUNCTION: CATALYZES THE FORMATION OF L-AMINOCYCLOPROPANE-1-
CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine -> L-
CC aminocyclopropane-1-carboxylate + methylthioadenosine.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS
CC MECHANICAL WOUNDING, A NUMBER OF CHEMICALS AND ANAEROBIOSIS.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PROSPHATE-DEPENDENT
CC AMINOTRANSFERASES.

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CC -----
DR EMBL; M88487; AAA03164.1; -
DR EMBL; X59146; AAA41857.1; -
DR EMBL; M63490; AAA34131.1; -
DR EMBL; M38705; AAA81381.1; -
DR PIR; A40960; A40960.
DR PIR; S19679; S19679.
DR HSP; P37821; I188.
DR Mendel; 511; LycEs; Acs; 4.
DR InterPro; IPR001176; ACo_synthase.
DR InterPro; IPR001511; AminoTran_1.
DR Pfam; PF00155; aminotran_1_2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSPEP_CLASS_1; 1.
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
KW Multigene family.
FT BINDING 282 282 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 15 15 V -> A (IN REF. 2).
FT CONFLICT 82 82 T -> A (IN REF. 4).
FT CONFLICT 253 253 S -> P (IN REF. 2).
SQ SEQUENCE 476 AA; 53537 MW; 9BC7D57BD64CB044 CRC64;

Query Match 61.9%; Score 1584; DB 1; Length 476;
Best Local Similarity 65.9%; Pred. No. 1e-114;
Matches 290; Conservative 72; Mismatches 72; Indels 6; Gaps 2;

QY 11 LLSKMAIGDGHGESSPYDGMKAYDONPHPTDNDPNVGMQGLAENOLTSDLVEDWILNN 70
DB 16 VLUSKLAQNEHQENSPYDGMKAYDONDPHLVNNJNGVQMLAENQLSVDLIEEWIKRN 75

QY 71 PEASICTPEGINDFRAINFQDYHGLAEFRNAVAKFARTGRNRTTFQDRIVMSGGATG 130
DB 76 PRASICTNDGIESFRANFQDYHGLPEETNAIAFMEKTRGGKVKFDKRVVMAGGATG 135

QY 131 AHEVTAFLADGCEAFPIPIYPYDGFDRDLRWRTQKVLVPVNCDSNNFVLTKEALEAD 190
DB 136 ANETILCLADPGDAFLPPTYPPYGNRDLWRSGVQLLPISCKSCNNFKITIEAEAY 195

QY 191 EKAREDNIRVKGLLTNTNSPLGTIMDRKTLRTVTVSFINEKRIHLVCDIEYAATVFSQP 250

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DB 196 EKGQOANVKIKGLIILTNPCNPLGTILDRDLTKKISTFTNEHNIHLVCDIEYAATVENSFK 255
QY 251 FTISAEIILEDFTDIECDRLNHLVHIVSLSKDMGFGPFRVCIYISYNDVAVNCARKWSSFL 310
DB 256 FVSIAEIINEDNCI--NKDHLHIVSSLSKDLGFGPFRVGIYISYNDVAVNCARKWSSFL 313
QY 311 VSTQTYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGGLAKVGIKCIQSAGLFLVMD 370
DB 314 VSTQTHLLAPMLSDDEFEVEELIESAKRLRERYEKFRGLEIGIKCLESNAGVYCWMD 373
QY 371 LRQLKKPTFTSETELWKVYIHEVKINVPSPGFSFCHTPEGFRVFCYANMDDMAYQIALQR 430
DB 374 LRSLLKEATLDAEMSLWKLIIINEVKLNVPSPGFSFCHTPEGFRVFCYANMDDMAYQIALQR 433
QY 431 IRNFV---LQNKVVVSNK 446
DB 434 IRNFMDAYNNVKNKNGVMKNK 453

RESULT 11
1A12_ARATH
ID 1A12_ARATH STANDARD; PRT; 496 AA.
AC Q06402;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 1-aminocyclopropane-2-carboxylate synthase 2 (EC 4.4.1.14) (ACC
GN AC52 QR ACC1 OR ATL601480 OR F22L4.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eumariophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustersids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=93028584; PubMed=1357670;
RA van der Straeten D., Rodrigues-Pousada R.A., Villarroel R., Hanley S.,
RA Goodman H.M., van Montagu M.;
RT "Cloning, genetic mapping, and expression analysis of an Arabidopsis
RL thaliana gene that encodes L-aminocyclopropane-1-carboxylate
RL synthase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:9969-9973(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=93066381; PubMed=1438312;
RA Liang X.-W., Abel S., Keller J.A., Shen N.F., Theologis A.;
RT "The L-aminocyclopropane-1-carboxylate synthase gene family of
RL Arabidopsis thaliana.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11046-11050(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Terry N.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.F.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

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RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
RT \*Sequence and analysis of chromosome 1 of the plant Arabidopsis  
thaliana.\*;  
RL Nature 408:816-820(2000).  
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-  
CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.  
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine - 1-  
aminocyclopropane-1-carboxylate + methylthioadenosine.  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- TISSUE SPECIFICITY: HIGH IN DEVELOPING LEAVES AND IN FLOWERS.  
CC -1- INDUCTION: BY ETHYLENE.  
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
AMINOTRANSFERASES.  
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CC -----  
DR EMBL; Z12614; CAA78260.1; -;  
DR EMBL; M95595; AAB59298.1; -;  
DR EMBL; M95594; AAA97516.1; -;  
DR EMBL; Y12776; CAA73310.1; -;  
DR EMBL; AC061957; AAF81308.1; -;  
DR PIR; S31646; S31646.  
DR PIR; A47199; A47199.  
DR PIR; S46190; S46190.  
DR HSP; P37821; 1B8G.  
DR Mendel; 15544; Arabid.Acs.mn15544.  
DR InterPro; IPR001170; ACC\_synthase.  
DR Pfam; PF00155; aminotran\_1.  
DR PRINTS; PR00753; ACCSYNTHASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;  
KW Multigene family.  
FT BINDING 279 279 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
FT VARIANT 136 136 M -> I.  
SQ SEQUENCE 496 AA; 55531 MW; 766318AE9B5F1566 CRC64;  
  
Query Match 61.7%; Score 1578; DB 1; Length 496;  
Best Local Similarity 59.8%; Pred. No. 3.2e-114;  
Matches 297; Conservative 82; Mismatches 102; Indels 16; Gaps 4;  
  
QY 1 MGFKAMDPTLLSKMAYGDGHGESSPYEDGWKAYDQNPHEPTDNPNGVMQGLAENOLTS 60  
DB 1 MGLPGKNGKAVLSKIATNNHGENSEYFDGWKAYDKDPFHLSRPHGLIQGLAENOLCL 60  
QY 61 DLVEDWTLNPEASICTPEGINDPRAIANFDYHGLAEFRNAVAKFMARTGRNRTFDPD 120  
DB 61 DLKDWKVENPEASICTLEGHQFSDIANFDYHGLAKKFKQATIAHFMKARGGRVTFDPE 120  
QY 121 RYVMSGGATGAHEVATCLADPGAFVLPIYPPGFRDRLWRRTGKVLVPMCDSSNFFV 180  
DB 121 RYVMSGGATGANETIMFCLADPGDFVLIPSPYAAAFDRDLWRRTGVIIIPVPCSSDNFK 180  
QY 181 LTKEALDEAYEKAREDNIRYKGLLITNPSNPLGTIMDKTLRTVVSFINKRIHLVDEI 240  
DB 181 LTVDAAEWATYKQAESKNKVGKLLITNPSNPLGTIMDKTLRTVVSFINKRIHLVDEI 240  
QY 241 YAATVSPQPGFISTAEILEDETIEDCRNLVHIYISLSDKMGFFGFRVGIYSNDVAVN 300  
DB 241 YAATVSPQPGFISTAEILEDETIEDCRNLVHIYISLSDKMGFFGFRVGIYSNDVAVN 300  
DB 241 YAATVFAGDGFVSVAEVNDVIDSEVNDLHIVISLSDKMGFLPGFRVGIYSNDVSVS 300

QY 301 CARMSFGLVSTOTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGGLAKVGIKQLQ 360  
DB 301 CARMSFGLVSSQTQLMASLSDQDFVDFLMESSRLGIRHKVFTTGGIKKADIACLT 360  
QY 361 SNAGLFVWMDLRQLLK-KPTFDSSETLWKVITHEVKINVSFGYFHCTEPGWFRVCYANM 419  
DB 361 SNAGLFVWMDLRQLLK-KPTFDSSETLWKVITHEVKINVSFGYFHCTEPGWFRVCYANM 420  
QY 420 DDMAVQIALQIRNFVLQNKVVV-----SNKKHCW-HSNLRSLKTRRDEDD 465  
DB 421 DDDTLHVALGRIQDFVSKNKNKIVEKASENDQVIONKSARKLKWQTQNLRLSFR-RLYED 479  
QY 466 ITMSPHPLPQSPVKA 482  
DB 480 GLSSPGIMSPHPLRA 496  
  
RESULT 12  
ID 1A1C\_MALDO STANDARD; PRT; 473 AA.  
AC P37821; Q40278; O04993;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC  
synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).  
GN ACS-1.  
OS Malus domestica (Apple) (Malus sylvestris).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.  
OX NCBI\_TaxID=3750;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CV. GOLDEN DELICIOUS; TISSUE=Fruit cortical tissue;  
RX MEDLINE-95232185; PubMed-7716231;  
RA Lay-Yee M., Knighton M.L.;  
RT "A full-length cDNA encoding 1-aminocyclopropane-1-carboxylate  
synthase from apple."  
RL Plant Physiol. 107:1017-1018(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CV. GOLDEN DELICIOUS;  
RA Harada T., Sunako T., Sakuraba W., Goto S., Senda M., Akada S.,  
RA Ishikawa R., Niizeki M.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 10-473 FROM N.A.  
RC STRAIN-CV. GOLDEN DELICIOUS; TISSUE=Fruit;  
RA Dong J.G., Kim W.T., Yip W.K., Thompson G.A., Li L., Bennett A.B.,  
RA Yang S.F.;  
RT "Cloning of a cDNA encoding 1-aminocyclopropane-1-carboxylate synthase  
and expression of its mRNA in ripening apple fruit."  
RL Planta 185:38-45(1991).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.37 ANGSTROMS).  
RX MEDLINE-20079531; PubMed-10610793;  
RA Capitani G., Hohenester E., Feng L., Storici P., Kirsch J.F.,  
RA Jansonius J.N.;  
RT "Structure of 1-aminocyclopropane-1-carboxylate synthase, a key  
enzyme in the biosynthesis of the plant hormone ethylene."  
RL J. Mol. Biol. 294:745-756(1999).  
CC -1- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-  
CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.  
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine - 1-  
aminocyclopropane-1-carboxylate + methylthioadenosine.  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.  
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
AMINOTRANSFERASES.  
CC -----



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DR EMBL; L31347; AAA73941.1; -;  
DR EMBL; U09156; AAB68617.1; -;  
DR EMBL; U03294; AAA03472.1; -;  
DR PDB; 1B8G; 26-JAN-00.  
DR Mendel; 251; MALDO; Acs:1.  
DR InterPro; 9005; MALDO; Acs:2.  
DR InterPro; IPR001176; ACC\_synthase.  
DR Pfam; PF00155; aminotran\_1.2; 1.  
DR PRINTS; PR00753; ACCSYNTHASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;  
KW Multigene family; 3D-structure.  
FT BINDING 273 273 PYRIDOXAL PHOSPHATE.  
FT CONFLICT 15 15 Q -> E (IN REF. 3).  
FT CONFLICT 101 101 E -> K (IN REF. 3).  
SQ SEQUENCE 473 AA; 53250 MW; 6ACA20759615E75D CRC64;

Query Match 52.4%; Score 1341; DB 1; Length 473;  
Best Local Similarity 53.0%; Pred. No. 5,6e-96;  
Matches 251; Conservative 83; Mismatches 126; Indels 14; Gaps 5;

QY 11 LLSKMAIGDHGESSPYFDGWKAYQONPHPTDNPNGVMQGLAENQLTSLDVEDWILNN 70  
DB 3 MLNRATNSHGQSDSYFLGWQYEKNPYHEVHNTNGIIQMGLAENQLDLESWLAKN 62  
QY 71 PEASICTPEGINDFRAIANFQDYGHLAEFRNAVAFMARTGRNRTEDPDRIVMSSGATG 130  
DB 63 PAAAFKNGESIFAEALFQDYGHLPAFKKAWDFMAEIRGNKVTFDPNHLVLTAGATS 122  
QY 131 AHEVTAFCIADPGAEFLVPIYPYPGFDRDLRWRTGKLVPMVCDSSNNFVLTKEALEDAY 190  
DB 123 ANETIFCLADPGAEALVPTPYPGFDRDLRWRTGVEIPIHCTSSNGFQITALEEAY 182  
QY 191 EKAREDNTRVGLLTNPNSPLGTTMDRKTLTIVVSYFNEKRIHLVDEIYAATVFSQPG 250  
DB 183 QBAERNLRVKGLVITNPNSPLGTTMTNELYLLLSFVEDKGIHLISDEIYSGTAFSSPS 242  
QY 251 FTISAEILEDETDIEDCRN-----LVHIVYSLSKDMGFPGRVGIYSYNDVAVNCARKM 305  
DB 243 FTSVMEVLKDR---NCDENSEVQVRVHVYSLSKDLGLGFGFVGAISYNDMDVVAATKM 299  
QY 306 SSFGLVSTQTOYLLASMLNDDSEVRFVLAESAKRLAQRFRVFTGGLAKVGKICLQSNAGL 365  
DB 300 SSFGLVSSQTOHLLSAMLSDKLTKNYTAENHKRLQKQKLVSLGSLQSGISCLNGAGL 359  
QY 366 FVWMDLRQLLKKPTDSETELKWKIIVHEVKNVSPGYSEFHCTEPGFRVCAVNDMDMAVQ 425  
DB 360 FCWDMRHLRLSTFAEMELMKKIVYEVHLNISPSSCHCTEPCGFRVCFANLPTERTID 419  
QY 426 IALQIRIRNFVLQNKVWV----SNKKHCWHSNLRSLKLTTRRDDTMTSPHSPLP 475  
DB 420 LAMQRLKAFVGYVYVPEVNGSQSSHLHSR-RQSL-TKKVSRSLSFDDRGPIP 471

RESULT 13  
ID 1A12\_CUCMA STANDARD; PRT; 475 AA.  
AC Q00257;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DE 15-DEC-1998 (Rel. 37, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase CMA101 (EC 4.4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).

GN ACS2 OR PCWAA.  
OS Cucurbita maxima (Pumpkin) (Winter squash).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eustoids I; Cucurbitales; Cucurbitaceae; Cucurbita.  
OX NCBI\_TaxID=3661;  
RP SEQUENCE FROM N.A.  
RA Nakagawa N., Kamiya Y., Imaseki H.;  
RT "Cloning of a complementary DNA for auxin-induced 1-aminocyclopropane-1-carboxylate synthase and differential expression of the gene by auxin and wounding.";  
RL Plant Cell Physiol. 32:1153-1163(1991).  
RN SEQUENCE FROM N.A.  
RA Nakagawa N., Kamiya Y., Imaseki H.;  
RT "Nucleotide sequence of an auxin-regulated 1-aminocyclopropane-1-carboxylic acid synthase gene from Cucurbita maxima Duch.";  
RL (In) Plant Gene Register PGR95-110.  
CC -|- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.  
CC -|- CATALYTIC ACTIVITY: S-adenosyl-L-methionine -|-  
CC 1-aminocyclopropane-1-carboxylate + methylthioadenosine.  
CC -|- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -|- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.  
CC -|- SUBUNIT: HOMODIMER.  
CC -|- INDUCTION: BY TISSUE WOUNDING AND AUXIN.  
CC -|- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.  
-----  
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DR EMBL; U37774; AAA91152.1; -;  
DR EMBL; D01033; BAA00839.1; -;  
DR PIR; JQ2214; JQ2214.  
DR HSSP; P37821; 1B8G.  
DR Mendel; 245; CUCma; Acs:2.  
DR InterPro; IPR001176; ACC\_synthase.  
DR InterPro; IPR001511; Aminotran\_1.  
DR Pfam; PF00155; aminotran\_1.2; 1.  
DR PRINTS; PR00753; ACCSYNTHASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;  
KW Multigene family.  
FT BINDING 272 272 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
SQ SEQUENCE 475 AA; 53481 MW; D02A666E137F44A0 CRC64;

Query Match 52.3%; Score 1339.5; DB 1; Length 475;  
Best Local Similarity 55.3%; Pred. No. 7.3e-96;  
Matches 246; Conservative 84; Mismatches 110; Indels 5; Gaps 3;

QY 11 LLSKMAIGDHGESSPYFDGWKAYQONPHPTDNPNGVMQGLAENQLTSLDVEDWILNN 70  
DB 3 MLNRATNSHGQSDSYFLGWQYEKNPYHEVHNTNGIIQMGLAENQLDLESWLAKN 62  
QY 71 PEASICTPEGINDFRAIANFQDYGHLAEFRNAVAFMARTGRNRTEDPDRIVMSSGATG 130  
DB 63 PDAASFRRKDGKSFRELALFQDYGHLPAFKKALVEFMAEIRGNKVSYFEANNVLTAGATS 122  
QY 131 AHEVTAFCIADPGAEFLVPIYPYPGFDRDLRWRTGKLVPMVCDSSNNFVLTKEALEDAY 190  
DB 123 ANETIFCLADPGAEALVPTPYPGFDRDLRWRTGVEIPIHCTSSNGFQITALEEAY 182  
QY 191 EKAREDNTRVGLLTNPNSPLGTTMDRKTLTIVVSYFNEKRIHLVDEIYAATVFSQPG 250  
DB 183 KDAQTRNLRVKGLVITNPNSPLGTTMTNRLDELNLVDFDFTSKGIHLISDEIYSGTVEGSPG 242



QY 251 FTSIAIELEDET--DIECDNLVHIVYSLSKOMGPFPGFRVGIISYNDVAVNCARKMSF 308  
 Db 243 FVSAMEVLKERSSEDEWVKR-VHIVYSLSKDGLGFRVGAISYNDMVAAATKMSF 301  
 QY 309 GLVSTQTYLLASMLNDDEFVERFLAESAKRLAQRPVFTGGGLAKVGIKQCSQAGLFW 368  
 Db 302 GLVSSQTYLLASMLNDKFTSYISENQKRLKQKMLVSLGKAGINCSDSNAGLFCW 361  
 QY 369 MDLRQLLKKPTDSETELWKVVIHEVKINVSQYSPCHTEPGFRVCIYANMDMAVOIAL 428  
 Db 362 VDMRHLLSDKFESELEMLKWKIVYVGLNISPSSCHCTEPGFRVCFANMSESTLKAV 421  
 QY 429 QRLRNFVLQNKVYVSNKKHCHSN 453  
 Db 422 RLKSFVTELRSTTSNHRN--HDN 444

RESULT 14  
 ID 1ALL\_ORYSA STANDARD; PRT; 487 AA.  
 AC Q07215;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE 1-aminocyclopropane-1-carboxylate synthase 1 (EC 4.4.1.14) (ACC  
 DE synthase 1) (S-adenosyl-L-methionine methylthioadenosine-lyase 1).  
 GN ACC1.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93283732; PubMed=8389618;  
 RA Zarembinski T.I., Theologis A.;  
 RT Anaerobiosis and plant growth hormones induce two genes encoding 1-  
 RT aminocyclopropane-1-carboxylate synthase in rice (*Oryza sativa* L.).\*;  
 RL Mol. Biol. Cell 4:363-373(1993).  
 CC -!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-  
 CC CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.  
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-  
 CC aminocyclopropane-1-carboxylate + methylthioadenosine.  
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.  
 CC -!- SUBUNIT: HOMODIMER.  
 CC -!- INDUCTION: BY ANAEROBIOSIS AND INDOLACETIC ACID (IAA) +  
 CC BENZYLADENINE (BA) + LICI1 TREATMENT.  
 CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----

DR EMBL; M96672; AAA33887.1; -;  
 DR EMBL; M96673; AAA33888.1; -;  
 DR HSP; P37821; I886.  
 DR InterPro; IPR001176; ACC\_synthase.  
 DR InterPro; IPR001511; Aminotran\_1.  
 DR Pfam; PF00155; aminotran\_1.2; 1.  
 DR PRINTS; PR00753; ACCSYNTHASE.  
 DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
 KW Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;  
 Multigene family.  
 FT BINDING 286 286 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 FT VARIANT 129 129 N -> T.  
 FT VARIANT 151 151 F -> L.

FT VARIANT 273 273 G -> D.  
 SQ SEQUENCE 487 AA; 53101 MW; 90FB80DEF3524009 CRC64;  
 Query Match 49.2%; Score 1258.5; DB 1; Length 487;  
 Best Local Similarity 53.9%; Pred. No. 1.3e-89;  
 Matches 236; Conservative 77; Mismatches 116; Indels 9; Gaps 4;  
 QY 5 AMDOTPLLSKMAIGDGHGSSPYFDGKWKAYQDNPFFHPTDNPNGVMQGLAENQJTSDLVE 64  
 Db 7 AEEKPQLLSKACGNSHGDSYFLGWQYEKNPFDVSNPSGIIQMGLEAENQLSFDLLE 66  
 QY 65 DWILNNPEASICTPE--GINDERAIANFODYHGLAEFRANAVAKEMARTGRNRTFDORI 122  
 Db 67 EWLEKNPALGRLREGGASVRELALFDYHGLPAEKNALARFMSQRGYKVVFDPSNI 126  
 QY 123 VMSGGATGAHEVTAFCIADPGAEFLVPIYPYPGDRDLRWRTGVKLVPMCDSSNNFVLT 182  
 Db 127 VLNAGATSAEALMFCIADHDAFFIPTYPYPGDRDLKWRGAEIVPVHCASANGFRVT 186  
 QY 183 KEALDAYEKAREDNIRKGLLTNPSPNPLGTINDRKLRTVTVSFINEKRIHLVCDEIYA 242  
 Db 187 RAALDDAYRAQKRRRLKVGVLITNPSPNPLGTASPRADLETIVDFVAAKGHILISDEIYA 246  
 QY 243 ATVFSOP--GFISTAEILEDETDEC--DRNLVHIVYSLSKOMGPFPGFRVGIISYND 297  
 Db 247 GTFAEPAGVSALEVVAGRDGGGAGVSDR--VHVYSLSKDGLGPGFRVGAISYND 304  
 QY 298 VVNCARKMSFGLVSTQTYLLASMLNDDEFVERFLAESAKRLAQRPVFTGGGLAKVGIK 357  
 Db 305 VVSAATKMSFGLVSSQTYLLAALLGDRDFTSRVVAENKRRKRIKRDQLVDGLREIGIG 364  
 QY 358 CLOSNAKGLFVMDLRQLLKKPTDSETELWKVVIHEVKINVSQYSPCHTEPGFRVCIYA 417  
 Db 365 CLPSNAGLCFWDMSHLMRSRSGFAGELMKVYVFEVGLNISPSSCHCTEPGFRVCF 424  
 QY 418 NMDDMAVOIALQRLNRFV 435  
 Db 425 NMSAKTLDVAMQRLRSFV 442

RESULT 15  
 ID 1AAT\_AQUAE STANDARD; PRT; 394 AA.  
 AC Q67781;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPAT).  
 GN ASPC OR AQ\_1969.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VF5;  
 RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aufay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus".  
 RL Nature 392:353-358(1998).  
 CC -!- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate = oxaloacetate +  
 CC L-glutamate.  
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1875.5	73.3	490	2	US-08-724-194-6	Sequence 6, Appli
2	1823	71.2	487	1	US-08-485-107-2	Sequence 2, Appli
3	1771.5	69.2	483	4	US-08-378-313-31	Sequence 31, Appli
4	1768	69.1	488	2	US-08-695-4128-10	Sequence 10, Appl
5	1755.5	68.6	485	4	US-08-378-313-30	Sequence 30, Appl
6	1713	66.9	485	4	US-08-378-313-27	Sequence 27, Appl
7	1713	66.9	485	4	US-08-378-313-32	Sequence 32, Appl
8	1710	66.8	485	4	US-08-378-313-25	Sequence 25, Appl
9	1702.5	66.5	482	2	US-08-724-194-5	Sequence 5, Appli
10	1698.5	66.4	482	2	US-08-724-194-4	Sequence 4, Appli
11	1637.5	64.0	493	4	US-08-378-313-19	Sequence 19, Appl
12	1636.5	64.0	493	4	US-08-378-313-21	Sequence 21, Appl
13	1636.5	64.0	493	4	US-08-378-313-28	Sequence 28, Appl
14	1627.5	63.6	494	4	US-08-378-313-23	Sequence 23, Appl
15	1627.5	63.6	494	4	US-08-378-313-29	Sequence 29, Appl
16	1578	61.7	496	2	US-08-463-418-2	Sequence 2, Appli
17	1563	61.1	476	4	US-08-378-313-34	Sequence 34, Appl
18	1514.5	59.2	371	3	US-09-043-627-10	Sequence 10, Appl
19	1430.5	55.9	365	3	US-09-043-627-8	Sequence 8, Appli
20	1393	54.4	368	3	US-09-043-627-4	Sequence 4, Appli
21	1374	53.7	366	3	US-09-043-627-6	Sequence 6, Appli
22	1333	52.1	360	3	US-09-043-627-2	Sequence 2, Appli
23	1299	50.8	469	4	US-08-378-313-33	Sequence 33, Appl
24	1006	39.3	323	4	US-08-846-826A-2	Sequence 2, Appli
25	971.5	38.0	324	2	US-08-860-577-8	Sequence 8, Appli
26	966	37.7	489	4	US-09-171-483-2	Sequence 2, Appli
27	871.5	34.1	289	4	US-08-846-826A-4	Sequence 4, Appli

Db 69 YLNNPQASICTAGQLEFKDRTAIFQDYHGLQSSDMLFANFMGKVRGNRVTFNPDRIVMG 128  
QY 127 GATGAHEVTAFCADPGEAFVPIPIYYPGDFDRDLAWRTGVKLVV-VMCDSSNNFVLTKEA 185  
Db 129 GATGAHEMTAFCLADPGDFAFLVPTPIYYPGDFDRDLAWRTGVPIVVVCESENFRITSA 188  
QY 186 LEDAYEKAREDIRYKGLLITNPSNPLGTIMDRKTLRTVVSFINBKRIHLVCDIYAATV 245  
Db 189 LBEAVERAQEDKIRYKGLLITNPSNPLGTILDRETLVSLVSPINEKNIHLVCDIYAATV 248  
QY 246 FSQPGFISATLEDETIEDCRNLVHIVISLSKDMGPPGFRVGIISYNDVAVNCARKM 305  
Db 249 FSQPAFVSIAEYIEQE-NVSCNRDLIHIIVISLSKDMGPPGFRVGIISYNDVAVNCARKM 307  
QY 306 SSGFLVSTQTYLLASMLNDDFEVFERFLAESAKRLAQFRVFTGGGLAKVIGKCLQSNAGL 365  
Db 308 SSGFLVSTQTYLLASMLNDDFEVFERFLAESAKRLARVFTTTRGLAQVNICLSNGGL 367  
QY 366 FVMDLRQLLKKPTFDETELWKVITHEVKINVSFGYSFHCTEPCGWFRVCYANMDDMAVQ 425  
Db 368 FIWMDLRLLKKEKTEAEAMLRVITNEVKLVNVSFGASPHCSEPCGWFRVCYANMDDMTMQ 427  
QY 426 IALORIRNVLONKEVWV--SNKKHCWHSNL-RLSLKTRRFDIT--MSPHSPLOSPM 479  
Db 428 VALRRIITFALQNKCAVLPALIKROCWMONNLGRLSLSRFRDFTMSPMSPHPI-QSPL 486  
QY 480 VKAT 483  
Db 487 VRAT 490

RESULT 2  
US-08-485-107-2  
; Sequence 2, Application US/08485107  
; Patent No. 5767376  
; GENERAL INFORMATION:  
; APPLICANT: STILES, JOHN I.  
; APPLICANT: NEUPANE, KABI R.  
; TITLE OF INVENTION: ACC SYNTHASE GENE AND ITS USE IN PLANTS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485.107  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: UH-01170  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415)705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-485-107-2

Query Match 71.2%; Score 1823; DB 1; Length 487;

Best Local Similarity 70.9%; Pred. No. 3.5e-194;  
Matches 339; Conservative 65; Mismatches 66; Indels 8; Gaps 3;  
QY 11 LLSKMAIGDGHGESSPYFDGWKAYQONPPHPTDNDNGVWQMGLAENQLTSLDVLVDILNN 70  
Db 10 LLSKIATSNHGHEDESPYFDGWKAYDSDPHPTQNPGEVITQMGLAENQLCFLNIHEWLLKN 69  
QY 71 PEASICTPEGINDFRAIANFQDYHGLAEPNNAVAKFMAKRNTRITFDPRIVMSGGATG 130  
Db 70 PEASICTAGAAEFEDIALFQDYHGLAEREAVAKFMKVRNRASFFDPRIVMSGGATG 129  
QY 131 AHEVTAFCADPGEAFVPIPIYYPGDFDRDLAWRTGVKLVPMCDSSNNFVLTKEALEDAY 190  
Db 130 AHEMTAFCLADPGDFAFLVPTPIYYPGDFDRDLAWRTGVKLVPMCDSSNNFVLTKEALEDAY 189  
QY 191 EKAREDNTRVKGILLITNPSNPLGTIMDRKTLRTVVSFINBKRIHLVCDIYAATVFSQPG 250  
Db 190 ETAQADIKVIGLLITNPSNPLGTITITDLEALVFTTNHKNHLVCDIYAATVFSQPG 249  
QY 251 FTISAEILEDETDIEDCRNLVHIVISLSKDMGPPGFRVGIISYNDVAVNCARKMSSFG 310  
Db 250 FTISAEIIE-EDKICNRDLIHIIVISLSKDMGPPGFRVGIISYNDVAVNCARKMSSFG 308  
QY 311 VSTQTYLLASMLNDDFEVFERFLAESAKRLAQFRVFTGGGLAKVIGKCLQSNAGLVWMD 370  
Db 309 VSSQTYLLASMLADDEFYDQFIVESKRLAMRHSFFFTQRLAQVINGICLKNAGLVWMD 368  
QY 371 LRQLLKKPTFDETELWKVITHEVKINVSFGYSFHCTEPCGWFRVCYANMDDMAVQIALOR 430  
Db 369 LRRLLEQTFEAEMLRVITNEIKLVNVSFGSSFCSEPCGWFRVCYANMDDMTMETALS 428  
QY 431 IRNFVLQNKREVVVSNKKHCWHSNLRLSLKTRRFDIT-----MSPHSPLOSPMVK 482  
Db 429 IKTFMLQHKAEAMVPMKKLQWQTSRLSLSPSS-RYEDIMETPGSFMSPHSPLOSPLVRA 485  
RESULT 3  
US-08-378-313-31  
; Sequence 31, Application US/08378313  
; Patent No. 6207881  
; GENERAL INFORMATION:  
; APPLICANT: THEOLOGIS, ATHANASIOS  
; APPLICANT: SATO, TAKAHIDO  
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH  
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378.313  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/862,493  
; FILING DATE: 02-APR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MORASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 29190-20002.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 856-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 483 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-378-313-31

Query Match 69.2%; Score 1771.5; DB 4; Length 483;  
Best Local Similarity 68.9%; Pred. No. 1.9e-188;  
Matches 326; Conservative 76; Mismatches 66; Indels 5; Gaps 3;  
  
QY 11 LLSKMAIGDGHGESSPYFDGKAYDQNPFPHTDNPNGVMOMGLAENOLTSDLVEDWLN 70  
DB 13 LLSKIATNDGHEGSPYFDGKAYDQNPFPHTDNPNGVMOMGLAENOLTSDLVEDWLN 72  
  
QY 71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAKFMARTGRNRTDPPDRIVMSGGATG 130  
DB 73 PKASICTVEGAENFQDIAIFQDYHGLPEFRQAVARFMEKVRGDRVTFDPNRIVMSGGATG 132  
  
QY 131 AHEVTAFLADPGAFVLPYYPGFDRLNWRGTVKLVPMCDSSNNFVLTKALEDAY 190  
DB 133 AHEMLAFCLADPGDAFLVPTYPYPGFDRLNWRGTVKLVPMCDSSNNFVLTKALEEAY 192  
  
QY 191 EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDIYAATVFSQP 250  
DB 193 EKAQSNIKIKGLLNPSNPLGTLDRKTLRTVVSFINKRIHLVCDIYAATVFSQP 252  
  
QY 251 FISTAEILEDETDIECDNRNLVHIYVSLSKDMGPFPGFRVGIYVSNVAVNCARKMSFGL 310  
DB 253 FISVSENVEM--TECTDLHIYVSLSKDLGFGFRVGIYVSNVAVNCARKMSFGL 310  
  
QY 311 VSTOTQYLLASMLNDDFEVERFLAESAKRLAQRVFTGGGLAKYGIKCLQSNAGLFWMD 370  
DB 311 VSTOTQYLLASMLNDDFEVERFLAESAKRLAQRVFTGGGLAKYGIKCLQSNAGLFWMD 370  
  
QY 371 LRQLLKPTDSETELAQVITHEVKINVSFCYSPCHCTEPGFRVFCYANMDDMAYQIALOR 430  
DB 371 LRLLKATDGELEWRLIINEVKLNVSFCSPCHCTEPGFRVFCYANMDDMAYQIALOR 430  
  
QY 431 IRNFVLQNKV--VYVSNKKHCHWSNLRLSKTRFRDDITMSPHPLPQSPMAVK 481  
DB 431 IRNFVLQTKLNNIAIKKQCSRSKLQISLFRLLDFNSPAHSPM-NSPLVR 482

RESULT 4  
US-08-695-412B-10  
; Sequence 10, Application US/08695412B  
; Patent No. 5874269  
; GENERAL INFORMATION:  
; APPLICANT: STILES, JOHN I.  
; APPLICANT: MOISYADI, STEFAN  
; APPLICANT: NEUPANE, KABI R.  
; TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT  
; TITLE OF INVENTION: DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE  
; TITLE OF INVENTION: RIPENING OF COFFEE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: JONES, DAY, REAVIS & POGUE  
; STREET: NORTH POINT, 901 LAKESIDE AVENUE  
; CITY: CLEVELAND  
; STATE: OHIO  
; COUNTRY: USA  
; ZIP: 44114  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS v. 5.1  
; SOFTWARE: Wordperfect v. 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/695,412B

; FILING DATE: 12-AUG-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US08/485,107  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRIFFITH, CALVIN P.  
; REGISTRATION NUMBER: 34,831  
; REFERENCE/DOCKET NUMBER: 265036600002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (216) 586-7050  
; TELEFAX: (216) 579-0212  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 488 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 178..1653  
; US-08-695-412B-10

Query Match 69.1%; Score 1768; DB 2; Length 488;  
Best Local Similarity 67.1%; Pred. No. 4.8e-188;  
Matches 325; Conservative 83; Mismatches 66; Indels 10; Gaps 5;  
  
QY 7 DOTLLSKMAIGDGHGESSPYFDGKAYDQNPFPHTDNPNGVMOMGLAENOLTSDLVEDW 66  
DB 8 EQOQLLSKMATNDGHEGSPYFDGKAYDSDPYHTRPNPGVIQMGLEAENOLCFLIEEW 67  
  
QY 67 ILNPEASICTPEGINDFRAIANFQDYHGLAEFRNAKFMARTGRNRTDPPDRIVMSG 126  
DB 68 VLNNPEASICTAEGANKFMEVAIYQDYHGLPEFRNAVARFMEKVRGDRVTFDPNRIVMSG 127  
  
QY 127 GATCAHEVTAFLADPGAFVLPYYPGFDRLNWRGTVKLVPMCDSSNNFVLTKALE 186  
DB 128 GATCAHEVTAFLADPGAFVLPYYPGFDRLNWRGTVKLVPMCDSSNNFVLTKALE 187  
  
QY 187 EDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDIYAATV 246  
DB 188 EAAVQKQAEANIRVKGFLNPNPLGTIVLDRETLIDITVFINKNHILICDEIYSATV 247  
  
QY 247 SQPGFISIAEILEDETDIECDNRNLVHIYVSLSKDMGPFPGFRVGIYVSNVAVNCARKMS 306  
DB 248 SQPEFISISEIIEH--DVQCNRLIHLVYSLSKDLGFGFRVGIYVSNVAVNCARKMS 305  
  
QY 307 SFGVSTOTQYLLASMLNDDFEVERFLAESAKRLAQRVFTGGGLAKYGIKCLQSNAGL 366  
DB 306 SFGVSTOTQYLLASMLNDDFEVERFLAESAKRLAQRVFTGGGLAKYGIKCLQSNAGL 365  
  
QY 367 VMMDLRQLLKPTDSETELAQVITHEVKINVSFCYSPCHCTEPGFRVFCYANMDDMAYQI 426  
DB 366 FWMDLRLLRESTEAEAMELWRLIINEVKLNVSFCSPCHCTEPGFRVFCYANMDDMAYQI 425  
  
QY 427 ALQIRNFVL-QNKV--VYVSNKKHCHWSNLRLSKTRFRDDITMSPHPLPQSPM 479  
DB 426 ALRRIHKFVLQVGKATEPTTPKSRGSKLQISLFRLLDFNSPAHSPM-ASPL 484  
  
QY 480 VKAT 483  
DB 485 VRAT 488

RESULT 5  
US-08-378-313-30  
; Sequence 30, Application US/08378313  
; Patent No. 6207881  
; GENERAL INFORMATION:  
; APPLICANT: THEOLOGIS, ATHANASIOS  
; APPLICANT: SATO, TAKAHIDO

; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH  
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,313  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/862,493  
; FILING DATE: 02-APR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 29190-20002.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 856-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 485 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-378-313-30

Query Match 68.6%; Score 1755.5; DB 4; Length 485;  
Best Local Similarity 68.8%; Pred. No. 1.2e-186;  
Matches 327; Conservative 76; Mismatches 65; Indels 7; Gaps 5;

QY 11 LLSKNAIGDGHGESSPYFDGWKAYQONPHPTDNPNGVQMGLAENQLTSDLVEDWILNN 70  
DB 13 LLSKIATNDGHSNPSYFDGWKAYANNPHPLTNDPTGTVMGLAENQLCFDLIQEWVNN 72  
QY 71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAFKFMARTGNRITFDPDRIVMSSGATG 130  
DB 73 PRASICTVEGAENFQDIAFQDYHGLPEFRQAVAFKFMKRGVDRVTFDPRIVMSGGATG 132  
QY 131 AHEVTAFCIADPGAEFLVPPIYPYPGFDRDLRWRTGVKLVPMCDSSNNFVLTKALEADAY 190  
DB 133 AHMLAFCLADPGDAFLVPTPIYPYPGFDRDLRWRTGVQLFPVVCESCNDFKVTTKALEEAY 192  
QY 191 EKAREDNIRVKGLLTNPNSPLGTIMDRKTLRTVVSFINEKRIHLVCDBIYAATVFSQPG 250  
DB 193 ERAQOSNIKIGLLINPNPLGTLTDKTLRDIIVTFINSKNIHLVCDBIYAATVFDQPR 252  
QY 251 FTISIAELDETDIECDRLNLIHVYSLSKDMGFPFGFRVGIYISYNDVAVNCARKMSSGL 310  
DB 253 FLSVSEIVEDM--IECNKDLIIHVYSLSKDLGFPFGFRVGIYISYNDTVVNIARKMSSFGL 310  
QY 311 VSTQTOYLLASLNDDEFVERFLAESAKRLAQFRVFTTGGAKVGIKCIQSNAGLFWVMD 370  
DB 311 VSTQTOHLLASLMSLDEVFIDKFAESSERLGERQGMFTKGLAEVGLSTLKSAGLFFWMD 370  
QY 371 LRQLKKPTFDSSETELWKVIIIEVKINVSFPGSFCTPGFGRVFCYANMMDMAVIALQR 430  
DB 371 LRRLKEATFSELELWRIIIEVKINLVNPGSCSFHCSEPGFGRVFCFANMDEFTMRALKR 430  
QY 431 IRNFVLQNEV--VVSNNKHKCHWSNLRSLKTRRED-DITMSP-HSPQSPMWK 481

DB 431 ISYFVLQPKGLNNAIAIKKQCSRRKLQISLSFRRLDHEFPMNSPAHSPM-NSPLVR 484  
RESULT 6  
US-08-378-313-27  
; Sequence 27, Application US/08378313  
; Patent No. 6207881  
; GENERAL INFORMATION:  
; APPLICANT: THEOLOGIS, ATHANASIOS  
; APPLICANT: SATO, TAKAHIDO  
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH  
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,313  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/862,493  
; FILING DATE: 02-APR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 29190-20002.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 856-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 485 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-378-313-27

Query Match 66.9%; Score 1713; DB 4; Length 485;  
Best Local Similarity 65.6%; Pred. No. 6.4e-182;  
Matches 319; Conservative 72; Mismatches 89; Indels 6; Gaps 4;

QY 1 MGFKAMDQTPLLSKNAIGDGHGESSPYFDGWKAYQONPHPTDNPNGVQMGLAENQLT 60  
DB 1 MGFETAKTNSIILSKLATNEEHGNSPYFDGWKAYSDPFPHLKPNPVGVIQMGLEAENQLCL 60  
QY 61 DLVEDWILNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAFKFMARTGNRITFDPD 120  
DB 61 DLIEDWIKRNPKGSCS--EGIKSFRAIANFQDYHGLPEFRKAIAKFMKTRGRVRFDE 119  
QY 121 RIVMSGGATGAHEVTAFCIADPGAEFLVPPIYPYPGFDRDLRWRTGVKLVPMCDSSNNFV 180  
DB 120 RYVMAGGATGANETIIFCLADPGDAFLVPSYPYAFNRLDRWRTGVQLPIHCSSNNFK 179  
QY 181 LTKALEADAYEKAREDNIRVKGLLTNPNSPLGTIMDRKTLRTVVSFINEKRIHLVCD 240  
DB 180 IYSKAVKEAYENRQAKSNIRKGLLTNPNSPLGTTLKDLKLSVLSFTNQHNHLVCD 239  
QY 241 YAATVFSQPGFISIAELETDIECDRLNLIHVYSLSKDMGFPFGFRVGIYISYNDVAVN 300  
DB 240 YAATVFDTPQFVSIAELDEQWTCNKDLHVIVYSLSKDMGLPGFRVGIYISFNDVYN 299



; MOLECULE TYPE: protein  
US-08-378-313-25

Query Match 66.8%; Score 1710; DB 4; Length 485;  
Best Local Similarity 65.6%; Pred. No. 1.4e-181;  
Matches 319; Conservative 71; Mismatches 90; Indels 6; Gaps 4;

QY 1 MGFKAMDTPLLSKMAIGDGHGESSPYFDGWKAYQDNPHPTDNPNGVMQGLAENQLTS 60  
DB 1 MGFEATKNSILSKLATNEEHGENSESPYFDGWKAYDSDPFHPLKPNGVQIMGLAENQLCL 60  
QY 61 DLVEDWILNPNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGRNITFPDP 120  
DB 61 DLIEDWIKRNPKGSICS-EGIKSPKAIANFQDYHGLPEFRKAIKFMETKTRGGRVREDPE 119  
QY 121 RIVMSGGATGAHEVTAFLADPGAEFLPIPIYPYFGFDRDLRWRTGVKLVPMCDSSNNFV 180  
DB 120 RVVMVGGATGANETIFFCLADPGDAFLVPSYYPAPFNRLRLWRRTGVQLIPICHESSNFK 179  
QY 181 LTKALEDAYEKAREDNIRVAGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDDEI 240  
DB 180 ITS KAVKAYENAKNSIKVKGLIITNPSNPLGTLTKSLVSTFQHNHILVCDDEI 239  
QY 241 YAATVFSOPGFSIAIEIIDEDETDICDRNLVHIVYSLSKDMGFGFRVGIYISYNDVYN 300  
DB 240 YAATVEDTPQFVSTAEIIDEQEMTYCNKDLVHIVYSLSKDMGLPGFRVGIYISFNDDVYN 299  
QY 301 CARMKSSFGLVSTQTYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGGLAKVGIKIQ 360  
DB 300 CARMKSSFGLVSTQTYFLAMLSDEKFDVDFLESARLGRKHFTNGLEVVGKICLK 359  
QY 361 SNAGFLVWMDLQLLKPTFSETELMKVHIVYSLSKDMGFGFRVGIYISYNDVYN 420  
DB 360 NNAGFLVWMDLQLLKPTFSETELMKVHIVYSLSKDMGFGFRVGIYISYNDVYN 419  
QY 421 DMVAOIALQRINFLVQNKVVSN---KKICW-HSNRLSLKTRRFDITMSP-HSPILP 475  
DB 420 DGTVDIALARRFRVGVSKGDKSSMEKKQMKNNRLSFSKRMVDESVLSPSSIP 479  
QY 476 OSPMVK 481  
DB 480 PSPLVR 485

RESULT 9  
US-08-724-194-5  
; Sequence 5, Application US/08724194  
; Patent No. 5824875  
; GENERAL INFORMATION:  
; APPLICANT: RANU, RAJINDER S.  
; TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE  
; TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS  
; TITLE OF INVENTION: IN GERANIUMS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SANTANGELO LAW OFFICES PC  
; STREET: 315 WEST OAK STREET, STE 701  
; CITY: FORT COLLINS  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80521  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,194  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANTANGELO, LUKE

; REGISTRATION NUMBER: 31,997  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (970) 224-3100  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 482 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-724-194-5  
  
Query Match 66.5%; Score 1702.5; DB 2; Length 482;  
Best Local Similarity 65.8%; Pred. No. 9.3e-181;  
Matches 312; Conservative 85; Mismatches 74; Indels 3; Gaps 3;  
  
QY 11 LLSKMAIGDGHGESSPYFDGWKAYQDNPHPTDNPNGVMQGLAENQLTSDLVEDWILNN 70  
DB 8 LLSKIATNDGHGENSEPYFDGWKAYDRDPFHPSONPVGVIQMGLEAENQLSSDLIEDWVRSN 67  
QY 71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGRNITFDPDRIVMSGGATG 130  
DB 68 PEASICTLEGVCKPKDVANFQDYHGLLEFRHAVAFAFMGRGKGVTFDDPRVVMGGPTG 127  
QY 131 AHEVTAFLADPGAEFLPIPIYPYFGFDRDLRWRTGVKLVPMCDSSNNFVLTKALEDAY 190  
DB 128 ANELIVFCLANPDGDAFLVPSYYPGNDRLQWRTGAQIIPVHCNSSNGPKITREALERSY 187  
QY 191 EKAREDNIRVAGLLITNPSNPLGTIMDRKTLRTVVSFINKRIHLVCDDEIYAATVFSOPG 250  
DB 188 AQAGSNIINLVKGLIITNPSNPLGTILDRDLTKLSIVSFVTDNNIHLVIDEIIYAATVFAPE 247  
QY 251 FTSIAIEIIDEDETDICDRNLVHIVYSLSKDMGFGFRVGIYISYNDVYNVNCARKMSSFG 310  
DB 248 FVSVSEILQEMDITCNPDLIHIVYSLSKDLGMPGFRVGIYISFNDDVYVSCARKMSSFG 307  
QY 311 VSTQTYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGGLAKVGIKIQSNAGLFVWMD 370  
DB 308 VSTQTYLLASMLNDEFEVERFLAES-RLGRRHGVFTKGLLELGTCLKSNAGLFVWMD 366  
QY 371 LRQLLKPTEFSETELMKVHIVYSLSKDMGFGFRVGIYISYNDVYNVNCARKMSSFG 430  
DB 367 LRKLEETFEAEVNLKVIINEVKNVSPGSSFHCVEPGRVCFANMDDTVHVALKR 426  
QY 431 IRNFVQNKVVSNKKHCHWSNRLSLKTRRFDITMSPHSPL-POSPMVK 482  
DB 427 IRAFVKGKVEGVPKRRKFMNDNLRLSFLSSRLAYDESVMLSPLHVMSPHSPLVRA 480

RESULT 10  
US-08-724-194-4  
; Sequence 4, Application US/08724194  
; Patent No. 5824875  
; GENERAL INFORMATION:  
; APPLICANT: RANU, RAJINDER S.  
; TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE  
; TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS  
; TITLE OF INVENTION: IN GERANIUMS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SANTANGELO LAW OFFICES PC  
; STREET: 315 WEST OAK STREET, STE 701  
; CITY: FORT COLLINS  
; STATE: CO  
; COUNTRY: USA  
; ZIP: 80521  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,194





;; APPLICANT: SATO, TAKAHIDO  
;; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH  
;; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS  
;; NUMBER OF SEQUENCES: 34  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 755 Page Mill Road  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304-1018  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/378,313  
;; FILING DATE:  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/862,493  
;; FILING DATE: 02-APR-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MURASHIGE, KATE H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 29190-20002.20  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 856-5600  
;; TELEFAX: (415) 494-0792  
;; TELEX: 706141  
;; INFORMATION FOR SEQ ID NO: 21:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 493 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-378-313-21

Query Match 64.0%; Score 1636.5; DB 4; Length 493;  
Best Local Similarity 63.0%; Pred. No. 2.2e-173;  
Matches 312; Conservative 74; Mismatches 96; Indels 13; Gaps 6;  
QY 1 MGFKAMDQ--TPLLSKMAIGDGHGSSPYFDGWKAYDONPHPTDNPNGVMOMGLAENOL 58  
DB 1 MGFHQIDERNQALLSKIALDDHGHGSSPYFDGWKAYDNDPFPENNPLGVQMGLAENOL 60  
QY 59 TSDLVEDWTLNNPEASICTPEGINDFRATIANFQDYHGLAEFRNAVAKFMARTGRNRTFD 118  
DB 61 SDFMIVDMIRKHPKPEASICTPEGLERFKSIANFQDYHGLPEFRNAIANFMGKVRGGRVKPD 120  
QY 119 PDRIVMSGGATGAHEVTAFCPLADPGAEAFVPIYPYPGFDRDLRWTGKVLVPMCDSSNN 178  
DB 121 PSRIVGGGATGASETIVFCLADPGDAFLVPSYAGDFDLKWRTRAQIIRVHCNRSNN 180  
QY 179 FVLTEADEAYEKAREDNIRVKGLLIITNPSNPLGTIMDRKTLRTVVSFINKEKRIHLVCD 238  
DB 181 FOVTKAALEIAVKKAEANMKVKGIITNPSNPLGTITDRTDLTKLTIVFNQDHLICD 240  
QY 239 ELYAATVVSQPCFISATLEDETIEDCRNIAVHIVSLSKDMGPPGPRVGIYISYNDAY 298  
DB 241 ELYSATVFKAPFTTSIAEIVEQME--HCKKELIHILYSLSKDMGLPGPRVGIYISYNDVY 298  
QY 299 VNCARMSFGVLVSTQTYLLASMLNDDFVERFLAEASAKRLAQRFRTVGTGLAKVGKIC 358  
DB 299 VRRARQMSFGVLVSTQTYLLASMLNDDFVERFLAEASAKRLAQRFRTVGTGLAKVGKIC 358  
QY 359 LOSNAGLFWMDLROLLKPTFDSSETELMKVIIHEVKINVSFGYSFHCTEPGWFRVCYAN 418  
DB 359 LNSNAGVFWMDLRLLLKQDTFKAEMELRWIINEVKLVNVSFGSSFHVTEPGWFRVCYAN 418  
QY 419 MDDMAVOIALQIRNFV--LQNK---VVVSNKKHCWHSNLR--SLKTRRFD--ITMS 469

DB 419 MDDNTVDVALNRIHSEVENIDKEDNTVAMPSTRHRONKRLSFSFGRRYDEGNVLNS 478  
QY 470 PHSPLPQSPVMKATN 484  
DB 479 PHTMSPHSPPLVIKN 493  
RESULT 13  
US-08-378-313-28  
;; Sequence 28, Application US/08378313  
;; Patent No. 6207881  
;; GENERAL INFORMATION:  
;; APPLICANT: THEOLOGIS, ATHANASIOS  
;; APPLICANT: SATO, TAKAHIDO  
;; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH  
;; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS  
;; NUMBER OF SEQUENCES: 34  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 755 Page Mill Road  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304-1018  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/378,313  
;; FILING DATE:  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/862,493  
;; FILING DATE: 02-APR-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MURASHIGE, KATE H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 29190-20002.20  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 856-5600  
;; TELEFAX: (415) 494-0792  
;; TELEX: 706141  
;; INFORMATION FOR SEQ ID NO: 28:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 493 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-378-313-28

Query Match 64.0%; Score 1636.5; DB 4; Length 493;  
Best Local Similarity 63.0%; Pred. No. 2.2e-173;  
Matches 312; Conservative 74; Mismatches 96; Indels 13; Gaps 6;  
QY 1 MGFKAMDQ--TPLLSKMAIGDGHGSSPYFDGWKAYDONPHPTDNPNGVMOMGLAENOL 58  
DB 1 MGFHQIDERNQALLSKIALDDHGHGSSPYFDGWKAYDNDPFPENNPLGVQMGLAENOL 60  
QY 59 TSDLVEDWTLNNPEASICTPEGINDFRATIANFQDYHGLAEFRNAVAKFMARTGRNRTFD 118  
DB 61 SDFMIVDMIRKHPKPEASICTPEGLERFKSIANFQDYHGLPEFRNAIANFMGKVRGGRVKPD 120  
QY 119 PDRIVMSGGATGAHEVTAFCPLADPGAEAFVPIYPYPGFDRDLRWTGKVLVPMCDSSNN 178  
DB 121 PSRIVGGGATGASETIVFCLADPGDAFLVPSYAGDFDLKWRTRAQIIRVHCNRSNN 180  
QY 179 FVLTEADEAYEKAREDNIRVKGLLIITNPSNPLGTIMDRKTLRTVVSFINKEKRIHLVCD 238  
DB 181 FOVTKAALEIAVKKAEANMKVKGIITNPSNPLGTITDRTDLTKLTIVFNQDHLICD 240

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QY 239 EIIAATVFSOPGFTIAEIILEDETDIECDORNLVHIIYVSLSKDMGPGFVRVGIISYNDAY 298
DB 241 EIIYSATVFKAPTFTSAIEIVEQME--HCKKELIHIIYLSKDMGLPGFVRVGIISYNDV 298
QY 299 VNCARKMSSEGLVSTQTYQLLASMLNDDEFVERFLAESAKRLAQFRVFTGGIAKVGKIC 358
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QY 359 LOSNAGLFWMDLRQLLKKRPTFDSFTELKWKVIIHEVKINVSFGYSPHCTEPGWFRVCYAN 418
DB 359 LNSNAGFWMDLRRLKKDQOTFKAEMELMRVINEYKLVNVSFSSPHVTEPGWFRVCYAN 418
QY 419 MDMVAOIALQRIRNFV--LQNKFE-----VVSNNKKHCWHSNLR--SLKTRRDD--ITMS 469
DB 419 MDMNTVDVALNRHISFVENIDKKEDNTVAMPSKTRHRDNKLRLSFSFSORRYDEGNVLS 478
QY 470 PHSPLPQSPMVKATN 484
DB 479 PHTMSPHSPLVIARN 493

RESULT 14
US-08-378-313-23
; Sequence 23, Application US/08378313
; Patent No. 6207881
; GENERAL INFORMATION:
; APPLICANT: THEOLOGIS, ATHANASIOS
; APPLICANT: SATO, TAKAHIDO
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,313
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29190-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 856-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-313-23

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Query Match 63.6%; Score 1627.5; DB 4; Length 494;  
Best Local Similarity 63.1%; Pred. No. 2.2e-172;  
Matches 311; Conservative . 73; Mismatches 96; Indels 13; Gaps 6;  
QY 1 MGFKANDQ--TPLLSKMAGDGHGCESSPYDGGWKAYDQNPFFHPDNPNGVMQGLAENQL 58

Db	1	MGFHQIDERNQALLXAIDDDGHEGNSATFDGKWAIDNNPFPENNPGLVIOGMAENQL	60
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Db	61	SFGMIVDWIRKHPEASICTPEGLEKFSIANFQDYHGLQEFRKAMASPMGKVGGRVKFD	120
Qy	119	PDRVMSGGATGAHEVTAFCIADPGGAFLVPDPYPGCFDRDLWRVTGKVLVPMVCDSSNN	178
Db	121	PSRIVMGGGATGASVTFICIADPGDAFLVPSPYAAFDRLKWRTRAQIIPVHCNSSNN	180
Qy	179	FVLTKEALEDAYEKAREDNTRVKGLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCD	238
Db	181	FQVTEARLEIAYKAGBANKVAGVIITNPSNPLGTYYORDTLKLVTFVNOHQDHLICD	240
Qy	239	EIYAATVFSOPGFSIAAEILDEDETDIECDRLNVHVIYSLSKDMGFGFVRGIIYSYNDAV	298
Db	241	EIYSATVEKAPTFTSIAEIVEQME--HCKKELHILYSLSKDMLGFGFVRGIIYSYNDAV	298
Qy	299	VNCARKMSSGLVSTQYQYLLASMLNDDPEVERFLAESAKRRAQRPVFTGGLAKVGIKC	358
Db	299	VRRAORSSFGVSSQTHLLAAMLSDDEDFVKFLAENSKRIGERHARTTKELDKMGITC	358
Qy	359	LOSNAGLFVMDLRQLLKKPTEDSETELAKVITHEVKINVSQYSPHCTEPCGWERVCYAN	418
Db	359	LNSNAGVFWMDLRLLKQDTFKAEMELRWIINEVKLNVSPGSSPHVTEPGWFRVCYAN	418
Qy	419	MDDMAVOIALQIRNFV--LQNE--VVSNNKKHCWHSNLR--SLKTRRED--DITMS	469
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Qy	470	PHSPLPOSMPVKA	482
Db	479	PHTMSPHSPLVRA	491

RESULT 15

US-08-378-313-29

; Sequence 29, Application US/08378313

; Patent No. 6207881

; GENERAL INFORMATION:

; APPLICANT: THEOLOGIS, ATHANASIOS

; APPLICANT: SATO, TAKAHD

; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH

; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/378,313

; FILING DATE:

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/862,493

; FILING DATE: 02-APR-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: MURASHIGE, KATE H.

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 29190-20002.20

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 856-5600

; TELEFAX: (415) 494-0792

; TELEX: 706141

RESULT 15  
US-08-378-313-29  
Sequence 29, Application US/08378313  
Patent No. 6207881  
GENERAL INFORMATION:  
APPLICANT: THEOLOGIS, ATHANASIOS  
APPLICANT: SATO, TAKAHIDO  
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH  
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,313  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/862,493  
FILING DATE: 02-APR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29, 959  
REFERENCE/DOCKET NUMBER: 29190-20002.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 856-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141

; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 494 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-378-313-29

Query Match		63.6%	Score 1627.5;	DB 4;	Length 494;
Best Local Similarity		63.1%	Pred. No. 2.2e-172;		
Matches	311;	Conservative	73;	Mismatches	96;
				Indels	13;
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QY	59	TSDLVEDRLNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFWARTGRNRTFD	118		
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QY	119	PDRIVMSGGATCAHEVTAFCIADPGCEALVPIPYYPGFDRLRWRTGVKLVPMGDSNN	178		
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QY	179	FVLTKEALEDAYEKAREDNIRVKLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCD	238		
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QY	239	EIYAATVFSQPGFISIAELLEDETDIECDRLVHIVYSLSKDMGPPGFRVGIYYSYNDAY	298		
Db	241	EIYSATVFKAPTFTSIAEIVEQME--HCKKELIHILYSLSKDMGLPGFRVGIYYSYNDV	298		
QY	299	VNCAKMSFGLVSTQTVLLASMLNDDDEFVERFLAESAKRLAQRVFTTGLAKVGIC	358		
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QY	359	LOSAGLFVMDLROLLKKPTFSETELWKVIIHEVKINVSFGYFCHTEPGWFRVCYAN	418		
Db	359	LNSNAGVFVMDLRLLLKQDTFKAEMLWRVINEVKLNVSFGSSFHVTEPGWFRVCYAN	418		
QY	419	MDMAVQIALORIRNV--LQNK---VVVSNKKHCWHSNRL--SLKTRFD--DITMS	469		
Db	419	MDNTVDVALNRHISFVENIDKKEDNTVAMPSTKTRHRONKRLKLSFSFGRRYDKGNVLNS	478		
QY	470	PHSPLPQSPMVKA	482		
Db	479	PHTMSPHSPLVRA	491		

Search completed: August 21, 2002, 02:08:53  
Job time: 4743 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 21, 2002, 02:01:05 ; Search time 42.72 Seconds  
(without alignments)  
1088.653 Million cell updates/sec

Title: US-09-763-957-2  
Perfect score: 2559  
Sequence: 1 MGFRAMDQTPLLSKMAIDG.....DITMSPHSLPQSPWKRATN 484  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR71:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	2354	92.0	484	2 S23002	1-aminocyclopropan
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4	1791.5	70.0	483	2 T02249	1-aminocyclopropan
5	1781.5	69.6	483	1 T07601	1-aminocyclopropan
6	1750.5	68.4	485	1 T07596	1-aminocyclopropan
7	1747.5	68.3	477	1 T04315	1-aminocyclopropan
8	1739.5	68.0	491	2 T03978	1-aminocyclopropan
9	1721	67.3	490	2 S31450	1-aminocyclopropan
10	1719.5	67.2	487	2 T50552	1-aminocyclopropan
11	1716	67.1	495	2 T13019	1-aminocyclopropan
12	1713	66.9	485	1 S19677	1-aminocyclopropan
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27	1521	59.4	370	2 T10513	1-aminocyclopropan
28	1483.5	58.0	421	2 T08119	1-aminocyclopropan
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30	1435	56.1	366	2 T07827	1-aminocyclopropan
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ALIGNMENTS

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N;Alternate names: ACC synthase  
C;Species: Vigna radiata (mung bean)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 03-Dec-1999  
C;Accession: S26214; S26213; S20919  
R;Botella, J.R.; Arteca, J.M.; Schlagnhauser, C.D.; Arteca, R.N.; Phillips, A.T.  
Plant Mol. Biol. 20, 425-436, 1992  
A;Title: Identification and characterization of a full-length cDNA encoding for an au  
of its mRNA in response to indole-3-acetic acid.  
A;Reference number: S26213; MUID:93043033  
A;Accession: S26214  
A;Molecule type: mRNA  
A;Residues: 1-484 <BOT>  
A;Cross-references: EMBL:Z11613; NID:g22069; PIDN:CAA77688.1; PID:g22070  
A;Experimental source: clone PAIM-1  
A;Accession: S26213  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 50-415, 'F', 417 <BOF>  
A;Cross-references: EMBL:Z11562; NID:g22067; PIDN:CAA77655.1; PID:g22068  
A;Experimental source: clone PHIM-1  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1992  
R;Botella, J.R.; Schlagnhauser, C.D.; Arteca, R.N.; Phillips, A.T.  
Plant Mol. Biol. 18, 793-797, 1992  
A;Title: Identification and characterization of three putative genes for 1-aminocyclo  
A;Reference number: S20919; MUID:92216056  
A;Accession: S20919  
A;Molecule type: DNA  
A;Residues: 27-94 <BOF>  
A;Cross-references: GB:M80554; NID:g170628; PIDN:AAA53297.1; PID:g170632  
A;Experimental source: Rwlilcz cv. Berken, etiolated hypocotyls; clone pMAC-1  
C;Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C;Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal pho  
F;279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match	100.0%	Score	2559;	DB	2;	Length	484;
Best Local Similarity	100.0%	Pred. No.	4.8e-196;				
Matches	484;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MGFRAMDQTPLLSKMAIDG	GSSPYFDGKAYDQNPFPHTDNPNGVMQGLAENQLTS	60			
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Db	61	DLVEDWTLLNPEASICTPEGINDFRAITAFQDHYGLAEFRNAKFMARTGRNRTITDPD	120				
QY	121	RIVMSGGATGAHEWTFACLDPGFAFLVPIPYPGFDRLRWRTGVKLVPMCDSSKNFV	180				

Db 121 RIVMSGGATGAHEVTAFCCLADPGEAFLVPIPYPGFDRDLRWRTGVKLVPMCDSSNFV 180  
Qy 181 LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTTLTVVSFNEKRIHLVCDIEI 240  
Db 181 LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTTLTVVSFNEKRIHLVCDIEI 240  
Qy 241 YAATVFSQPGFISIAIELEDIEDCDRLNHLVIVYSLSKDMGFGFRVGIISYNDVAVN 300  
Db 241 YAATVFSQPGFISIAIELEDIEDCDRLNHLVIVYSLSKDMGFGFRVGIISYNDVAVN 300  
Qy 301 CARMKSSFGVLSTQTOYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGLAKVGKICLQ 360  
Db 301 CARMKSSFGVLSTQTOYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGLAKVGKICLQ 360  
Qy 361 SNAGLFVWMDLRQLLKKPTFDESETELWKVIIHEVKINVSFGYSFHCTEPGWFRVCYANMD 420  
Db 361 SNAGLFVWMDLRQLLKKPTFDESETELWKVIIHEVKINVSFGYSFHCTEPGWFRVCYANMD 420  
Qy 421 DNVAOIALQIRIRNFVQLQNEVVVSNKKHCWHSNLRSLKTRFRDDITMSPHSPLPQSPMV 480  
Db 421 DNVAOIALQIRIRNFVQLQNEVVVSNKKHCWHSNLRSLKTRFRDDITMSPHSPLPQSPMV 480  
Qy 481 KATN 484  
Db 481 KATN 484  
RESULT 2  
S25002  
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - soybean  
C:Species: Glycine max (soybean)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 04-Feb-2000  
C:Accession: S25002  
R:Li, D.; Li, N.; Mattoo, A.K.  
A:Description: Nucleotide sequence of soybean ACC synthase.  
A:Reference number: S25002  
A:Accession: S25002  
A:Molecule type: mRNA  
A:Residues: 1-484 <LIU>  
A:Cross-references: EMBL:X67100; NID:g18557; PIDN:CAA47474.1; PID:g18558  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosphate  
F:279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 92.0%; Score 2354; DB 2; Length 484;  
Best Local Similarity 90.9%; Pred. No. 1.1e-179;  
Matches 439; Conservative 21; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTS 60  
Db 1 MGLMDVDQTPQLLSKMWIGDGHGESSPYFDGWKAYDENPFPKPNPNGVIQMGLAENQLTS 60  
Qy 61 DLVEDWILNPNPASICTEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGRNRTTFDDP 120  
Db 61 DLVEDWILNPNPASICTEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGRNRTTFDDP 120  
Qy 121 RIVMSGGATGAHEVTAFCCLADPGEAFLVPIPYPGFDRDLRWRTGVKLVPMCDSSNFV 180  
Db 121 RIVMSGGATGAHEVTAFCCLADPGEAFLVPIPYPGFDRDLRWRTGVKLVPMCDSSNFV 180  
Qy 181 LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTTLTVVSFNEKRIHLVCDIEI 240  
Db 181 LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTTLTVVSFNEKRIHLVCDIEI 240  
Qy 241 YAATVFSQPGFISIAIELEDIEDCDRLNHLVIVYSLSKDMGFGFRVGIISYNDVAVN 300  
Db 241 YAATVFSQPGFISIAIELEDIEDCDRLNHLVIVYSLSKDMGFGFRVGIISYNDVAVN 300  
Qy 301 CARMKSSFGVLSTQTOYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGLAKVGKICLQ 360  
Db 301 CARMKSSFGVLSTQTOYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGLAKVGKICLQ 360  
Qy 421 DNVAOIALQIRIRNFVQLQNEVVVSNKKHCWHSNLRSLKTRFRDDITMSPHSPLPQSPMV 480  
Db 421 DNVAOIALQIRIRNFVQLQNEVVVSNKKHCWHSNLRSLKTRFRDDITMSPHSPLPQSPMV 480

Qy 361 SNAGLFVWMDLRQLLKKPTFDESETELWKVIIHEVKINVSFGYSFHCTEPGWFRVCYANMD 420  
Db 361 SNAGLFVWMDLRQLLKKPTLDESEMELRWIIDEVKINVSFGSFHCTEPGWFRVCYANMD 420  
Qy 421 DNVAOIALQIRIRNFVQLQNEVVVSNKKHCWHSNLRSLKTRFRDDITMSPHSPLPQSPMV 480  
Db 421 DNVAOIALQIRIRNFVQLQNEVVVSNKKHCWHSNLRSLKTRFRDDITMSPHSPLPQSPMV 480  
Qy 481 KAT 483  
Db 481 KAT 483  
RESULT 3  
T06253  
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 2 - garden pea  
C:Species: Pisum sativum (garden pea)  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 11-May-2000  
C:Accession: T06253  
R:Peck, S.C.; Kende, H.  
A:Title: Differential regulation of genes encoding 1-aminocyclopropane-1-carboxylate  
A:Reference number: Z15569; MUID:99084749  
A:Accession: T06253  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-487 <PEC>  
A:Cross-references: EMBL:AF016459; NID:g2360988; PIDN:AAD04199.1; PID:g2360989  
C:Genetics:  
A:Gene: ACS2  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosphate  
F:279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 82.7%; Score 2115.5; DB 2; Length 487;  
Best Local Similarity 81.1%; Pred. No. 1.1e-160;  
Matches 394; Conservative 47; Mismatches 42; Indels 3; Gaps 2;

Qy 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDONPFPHTDNPNGVMQGLAENQLTS 60  
Db 1 MGVWMLDQTPQLLSKIAMGDGHGESSPYFDGWKAYDKDPHPKSNPHGVIQMGLAENQLTA 60  
Qy 61 DLVEDWILNPNPASICTEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGRNRTTFDDP 120  
Db 61 DMVQNMINSPEASICTLEGVHNFQMANFQDYHGLPEFRNAVAKFMSTRGRNRTTFDE 120  
Qy 121 RIVMSGGATGAHEVTAFCCLADPGEAFLVPIPYPGFDRDLRWRTGVKLVPMCDSSNFV 180  
Db 121 RIVMSGGATGAHEVTAFCCLADPGEAFLVPTPYPGFDRDLRWRTGVKLVPMCDSSNFV 180  
Qy 181 LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRKTTLTVVSFNEKRIHLVCDIEI 240  
Db 181 LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTTMDRNTLRTVITFINEKRIHLISDEI 240  
Qy 241 YAATVFSQPGFISIAIELEDIEDCDRLNHLVIVYSLSKDMGFGFRVGIISYNDVAVN 300  
Db 241 YAATVFSHPFSFISIAIEIIEHDIEDCDRLNHLVIVYSLSKDMGFGFRVGIISYNDVVD 300  
Qy 301 CARMKSSFGVLSTQTOYLLASMLNDEFEVERFLAESAKRLAQRFRVFTGGLAKVGKICLQ 360  
Db 301 CTRKMSSEGLVSTQTOYLLAKMLSDDDPVERKLSAKRLAQRVFTGGLKLVGKICLQ 360  
Qy 361 SNAGLFVWMDLRQLLKKPTFDESETELWKVIIHEVKINVSFGYSFHCTEPGWFRVCYANMD 420  
Db 361 SNGLFVWMDLRGLLKNATFESEIELRWVIIHEVKINVSFGYSFHCSEPGWFRVCYANMD 420  
Qy 421 DNVAOIALQIRIRNFVQLQ-NKEVVS--NKKHCWHSNLRSLKTRFRDDITMSPHSPLPQS 477  
Db 421 DRDVOIALQIRIRSFVTQNNKEAMGSKNSKPYWHWSNLRSLKPRRFRDDITMSPHSPIPQS 480  
Qy 478 PMVKAT 483

Db 481 PLVRAT 486

1:|||||

RESULT 4  
T02249

1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - common tobacco  
N:Alternate names: ACC synthase  
C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 20-Jun-2000  
C:Accession: T02249  
R:Weterings, K.; Perzotti, M.; Cornelissen, M.; Mariani, C.  
Submitted to the EMBL Data Library, June 1996  
A:Description: Pollination induced ACC-synthase and ACC-oxidase expression.  
A:Reference number: Z14638  
A:Accession: T02249  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-483 <WET>  
A:Cross-references: EMBL:X98492; PIDN:CAA67118.1  
C:Genetics:  
A:Gene: ACCS2  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph  
F:278/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match	70.08;	Score	1791.5;	DB	2;	Length	483;
Best Local Similarity	68.1%;	Pred.	No. 7.5e-135;				
Matches	329;	Conservative	79;	Mismatches	72;	Indels	3;
Gaps							

  

Qy	1	MGFKAMDOTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFFHTDPNPGVMQMGLAENQLTS	60
Db		:       :       :       :       :       :       :	
Qy	1	MGFISSIDNELLSKVATNNNGENSAYSFDGWKAYEIDPFPHPTQNSDGVIONGLAENLCF	60
Db		:       :       :       :       :       :       :	
Qy	61	DLVEDWILNNPEASICTPEGINDIRAJANFODYHGLEAFNRNAVAKFMARTRGNRIITDPD	120
Db		:       :       :       :       :       :       :	
Qy	61	DLIOEWVVKPKASICTAEGSQDFKDAIYODYHGLEPFRSAAVAREMKGVRGDRIITEPE	120
Db		:       :       :       :       :       :       :	
Qy	121	RIVMSGGATGAHEVTATCLADPGBAFLVPYPYPGGPDRDLRWRTGVKLVPVWCDOSSNFV	180
Db		:       :       :       :       :       :       :	
Qy	121	RIVMSGGATGAHELLEACLADPGEAFTLVPTYPYPGGPDRDLRWRTGVOLFPPVCSESSNFK	180
Db		:       :       :       :       :       :       :	
Qy	181	LTRKALDAYEKAREDNI RVKGLLIITNPSPLGTIMDKRLT RTVVSTINEKRHIHLVDEI	240
Db		:       :       :       :       :       :       :	
Qy	181	VTKRALPAAYCKAQESNITVKGLLNLNPNPLGTILORETLKDYRVFINEKNHILVDEI	240
Db		:       :       :       :       :       :       :	
Qy	241	YAATVFSPQPGFISIAELEDETIECDRNLVHVIYVSLSKDMGFPGRVGIYYSYNDAVVN	300
Db		:       :       :       :       :       :       :	
Qy	241	YAATIFNKPDFISISVIMEE-DVECDRDLIHVYSLSKDLGPPGPRVGIYYSYNDVVTN	299
Db		:       :       :       :       :       :       :	
Qy	301	CARKMSFGLYSTOTQYLASMLNDDFEVERFLAESAKRLAQRFRVTTGGGLAKVGICLQ	360
Db		:       :       :       :       :       :       :	
Qy	300	CARKMSFGLYSTOTQELINMLSDENFVTKFIGESSERLQKRHGMEFTRGLAQVGINLK	359
Db		:       :       :       :       :       :       :	
Qy	361	SNAGLFVMDLRQLLKPTDFSETELAKVIIIEHKVINVSFCYSFHCTPCGFWRFCYANMD	420
Db		:       :       :       :       :       :       :	
Qy	360	SNAGLFVMDLRULLKEUFPAAELUELRILIINEVKLVNPGSCSPHCSEPGFRVCFANMD	419
Db		:       :       :       :       :       :       :	
Qy	421	DMAYOIALQRINREVLANKEVVVSNKK-HCWHWSNLRLSLKTRRRDDITMSHPSPLOSPM	479
Db		:       :       :       :       :       :       :	
Qy	420	DETHRIALRRINNEVIOBKIEGGVKKLOCRSKLETSLSFRLKLDPMNSPHSPM-SSPL	478
Db		:       :       :       :       :       :       :	
Qy	480	VKA	482
Db			
Qy	479	VOA	481
Db			

submitted to the EMBL data library, September 1990  
A:Description: LE-ACS1A and LE-ACS1B, duplicated genes encoding 1-aminocyclopropane-1  
A:Reference number: Z16039  
A:Accession: T07596  
A:Status: translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA

A:Residues: 1-485 <OON>  
A:Cross-references: EMBL:U72389; NID:g1621640; PIDN:AAB17278.1; PID:g1621641  
A:Experimental source: cultivar Rutgers; clone PLEACSIa3  
C:Genetics:  
A:Gene: ACS1A  
C:Function:  
A:Description: catalyzes the conversion of S-adenosylmethionine to 1-aminocyclopropane-1-carboxylate  
A:Pathway: ethylene biosynthesis  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph  
F:279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

	Query Match	Best Local Similarity	Score	DB 1;	Length	DB 2;
	Matches	Conservative	326;	Mismatches	66;	Indels
						Gaps
Qy	11	LLSKWATGDHGESSPFYDGKWKAYDQNPFIPTDNPNGVMQGLAENQLTSLDVEDWILNN	70			
Db	13	LLSKIATNDHGESSPFYDGKWKAYANNPFIPTDNPNGVMQGLAENQLTSLDVEDWILNN	72			
Qy	71	PEASICTPEGINDFRATANFQDYHGLAEFRNAVAKFMAATRGNRITTFDPRDRLVMSGGATG	130			
Db	73	PKASICTVEGAENFQDIAFDQYHGLPEFRQAVAREMEKVRGDRVTFDPNRIYVMSGGATG	132			
Qy	131	AHEVTAFLADPGAEFLVPIPYEGFDRDLRWRTGVLKVPVCMDSNNFVLTKALEADAY	190			
Db	133	AHEMLAFCLADPGDAFLVPTPYPCGDRDLRWRTGVLKFPVVCESCDNFVTKALEADAY	192			
Qy	191	EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVVFINEKRIHLVCDIEYAATVFSQPG	250			
Db	193	EKAQSNIRKIGLLINPNPLGTILDKDTRDIVTFINSKNIHLVCDIEYAATVFSQPG	252			
Qy	251	FISIAEILEDFTEDCDRLNLIHVIVSLSKDMGFGFGRVGIIVSYNDVAVNCARKMSSFGL	310			
Db	253	FISVSEIVEDM--TECKNOLDLIHVIVSLSKDGLGFGFGRVGIIVSYNDVAVNCARKMSSFGL	310			
Qy	311	VSTQTVLLASMLNDEDFVERFLAESAKRLAQRFRVFTGGGLKVGIKLQSNAGLVFVMD	370			
Db	311	VSAQTQHLASMLNDEDFVDFDKFAESSRIGERQGMFTKGLAEVGIISTLKSNAGLVFWMD	370			
Qy	371	LROLLKPTDFSEFELWKVITHEKVINSPGYSHCTEPGHWFRVCYANMDDMAVOIALQR	430			
Db	371	LRLLEKATDFSELELWRITIIINEVKLVNSPCGSHCEPGEHWFRVCYANMDDMETIALKR	430			
Qy	431	IRNFVLQNKVE--VVSNNKHCWHSNLRSLSLKTRFED-DITMSP-HSPLPQSPMVK	481			
Db	431	ISYFVLQPKGLNNIAAKQCSRKLQISLFRRLDHEFMNSPAHSPM-NSPLVR	484			

RESULT 7  
T04315  
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - tomato  
N:Alternate names: ACC synthase; S-adenosyl-L-methionine methylthioadenosine-lyase  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 16-Jun-2000  
C:Accession: T04315  
R:Nakajima, N.; Bae, G.; Saji, H.; Aono, M.; Kubo, A.; Kondo, N.  
submitted to the EMBL Data Library, April 1998  
A:Description: Rapid accumulations of transcripts of ethylene biosynthesis enzymes in  
A:Reference number: Z15278  
A:Accession: T04315  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-477 <NAK>  
A:Cross-references: EMBL:AB013346; PIDN:BAZ5916.1  
A:Experimental source: tissue-type green leaves  
C:Function:  
A:Description: catalyzes the conversion of S-adenosylmethionine to 1-aminocyclopropane-1-carboxylate  
A:Pathway: ethylene biosynthesis  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph  
F:269/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted



Db 121 RVVMAGGATGANETIIIFCLADTGDALFVPSYPYPAFNRLRWRTGVQLIIPCDSSNNFQ 180  
QY 181 LTVKEALEDAYEKAREDIRVKGILLTNPSNPLGTIMDRKTLRTVWSPINERKIRHLVCEDEI 240  
Db 181 ITTKAVREAYENAQKSNIKVGLILTNPSNPLGTITLDRDTLKNLLTFTQNHNLHLVCEDEI 240  
QY 241 YAATVFSQPGFISATLEDETIEDCRNLVHIVISLSKDMGPGFVRVGIYISYNDVAVN 300  
Db 241 YAATVNTPOFVSIAETLDDTS-HCNKDLVHIVISLSKDMGLPGFVRVGIYISYNDVAVN 299  
QY 301 CARMSFGLVSTQTOYLLASMLNDDFEVERFLAESAKRLAQFRVFTGGGLAKVIGIKLQ 360  
Db 300 CARMSFGLVSTQTOYLLAEMLSDERFVSFLTSSKRLAKRKHFTNGLEEVGIKCLR 359  
QY 361 SNAGLFVMDRLQLKKPTDSETELWKVIIHEVKINVSFGYSPHCTEPGWFRVCYANMD 420  
Db 360 SNAGLFVMDRLQLKKPTDSETELWKVIIHEVKINVSFGYSPHCTEPGWFRVCYANMD 419  
QY 421 DMVAOIALORIRNFVLQNK-----VVVSNKKHCW-HSNLRLSLKTRRFD-ITMSP-HS 472  
Db 420 DETVDALARIRFVGKKSDESTPILMEKQKNNLRLSFRKMYDESVLSPSS 479  
QY 473 PLPQSPMVK 482  
Db 480 PIPHSPLVRA 489

## RESULT 9

S31450  
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - garden petunia  
C:Species: Petunia x hybrida (garden petunia)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 04-Feb-2000  
C:Accession: S31450  
R:Michael, M.Z.; Baudinette, S.C.; Savin, K.W.; Cobbett, C.S.; Cornish, E.C.  
submitted to the EMBL Data Library, December 1992  
A:Description: Isolation of petal senescence-associated cDNA clones encoding 1-aminocyclopropane-1-carboxylate synthase  
A:Reference number: S31450  
A:Accession: S31450

A:Molecule type: mRNA  
A:Residues: 1-490 <MIC>

C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase

C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosphate  
F:278/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 67.3%; Score 1721; DB 2; Length 490;  
Best Local Similarity 65.4%; Pred. No. 3.2e-129;  
Matches 320; Conservative 73; Mismatches 88; Indels 8; Gaps 4;

QY 1 MGPKAMDQTPLLSKMAIGDGHGSSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTS 60  
Db 1 MGPESEKNNSVLSKLTATNEEGHNSPYFDGWKAYDNDPFPKLPNGVIOQGLAENQLCF 60  
QY 61 DLVEDTLNPNESICTPEGINDFRATNFQDYHGLAEFRNAVAKFARTGRNITFDPD 120  
Db 61 DLLEDWIKRNPASICTTEGIKSFRGTANFQDYHGLAEFRNAVAKFARTGRNITFDPD 120  
QY 121 RYVMSGGATGAHEVTAFCLADPGAEFLVPIYPYPGFDRDLRWRTGVKLVPMVDCSSNNFV 180  
Db 121 RVVMAGGATGANETIIIFCLADAGDALFVPSYPYPAFNRLRWRTGVQLIIPCESSNFK 180  
QY 181 LTVKEALEDAYEKAREDIRVKGILLTNPSNPLGTIMDRKTLRTVWSPINERKIRHLVCEDEI 240  
Db 181 ITTKAMKEAYENAIKARIRVKGILLTNPSNPLGTITLDRDTLKNLLTFTQNHNLHLVCEDEI 240  
QY 241 YAATVFSQPGFISATLEDETIEDCRNLVHIVISLSKDMGPGFVRVGIYISYNDVAVN 300  
Db 241 YAATVNTPOFVSIAETLDDTS-HCNKDLVHIVISLSKDMGLPGFVRVGIYISYNDVAVN 299  
QY 301 CARMSFGLVSTQTOYLLASMLNDDFEVERFLAESAKRLAQFRVFTGGGLAKVIGIKLQ 360

Db 300 CARMSFGLVSTQTOYLLAKMLSDSEEFVANFLCESSMRLGKRKHFTNGLEEVGIKCLR 359  
QY 361 SNAGLFVMDRLQLKKPTDSETELWKVIIHEVKINVSFGYSPHCTEPGWFRVCYANMD 420  
Db 360 SNAGLFVMDRLQLKKPTDSETELWKVIIHEVKINVSFGYSPHCTEPGWFRVCYANMD 419  
QY 421 DMVAOIALORIRNFVLQNK-----VVVSNKKHCW-HSNLRLSLKTRRFD-ITMSP-HS 472  
Db 420 DETVEALARIRFVGKVGKENGEBTPVKNKQKNNLRLSFRKMYDESVLSPSS 479  
QY 474 LPQSPMVK 482  
Db 480 IPHSPLVRA 488

## RESULT 10

T50552

1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) acsl [similarity] - white lupine  
C:Species: Lupinus albus (white lupine)

C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 03-Nov-2000  
C:Accession: T50552

R:Bekman, E.P.; Saibo, N.J.M.; Di Cataldo, A.; Regalado, A.; Pinto Ricardo, C.; Rodri  
submitted to the EMBL Data Library, January 1999

A:Description: Four genes encoding 1-aminocyclopropane-1-carboxylate synthase in Lupi  
A:Reference number: 225126

A:Accession: T50552

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-487 <BEK>

A:Cross-references: EMBL:AF119411; PIDN:AAF22109.1

C:Genetics:

A:Gene: ACS1

A:Introns: 56/3; 100/3; 154/2

C:Function:

A:Pathway: ethylene biosynthesis

C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase

C:Keywords: carbon-sulfur lyase; phosphoprotein; pyridoxal phosphate

F:277/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 67.2%; Score 1719.5; DB 2; Length 487;  
Best Local Similarity 66.3%; Pred. No. 4.2e-129;  
Matches 320; Conservative 74; Mismatches 74; Indels 15; Gaps 5;

QY 11 LLSKMATGDCGHGSSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTSLDVEDTLNN 70

Db 10 LLSKIATNDKRGNSPYFDGWKAYDNNPFPKPNPQVIOQGLAENQLCFDLEEWIKNN 69

QY 71 PEASICTPEGINDFRATNFQDYHGLAEFRNAVAKFARTGRNITFDPDRIVMSGGATG 130

Db 70 PKASICTLEGVHKFRDIFANFQDYHGLAEFRNAVAKFARTGRNITFDPDRIVMSGGATG 129

QY 131 AHEVTAFCLADPGAEFLVPIYPYPGFDRDLRWRTGVKLVPMVDCSSNNFVLTKEALEDAY 190

Db 130 ANEVIMECLADPGDALFVPTPYPAFLDLRWRTGLQILPVECDSSNNFKITREALEKAY 189

QY 191 EKAREDIRVKGILLTNPSNPLGTIMDRKTLRTVWSPINERKIRHLVCEDEIYAATVFSQPG 250

Db 190 NKAKEDINVKGLITNPSNPLGTITLDRDLKSLITFINENNNHIVCEDEIYAATVFSQPS 249

QY 251 FISTAEILEDETIEDCRNLVHIVISLSKDMGPGFVRVGIYISYNDVAVNCAKMSFGL 310

Db 250 YVSVSEDIQ-EMQPCCKDLHIIISLSDMGPGFVRVGIYISYNDVAVNCAKMSFGL 308

QY 311 VSTQTOYLLASMLNDDFEVERFLAESAKRLAQFRVFTGGGLAKVIGIKLQSNAGLFVMD 370

Db 309 VSSQTOHMLASMLSDSDSFVDKFLAESKKRLAKRHNIFSKVLEEVNITKFPNSNAGLFVMD 368

QY 371 LRQLKKPTDSETELWKVIIHEVKINVSFGYSPHCTEPGWFRVCYANMDMAVOIALQR 430

Db 369 LKSLLEKQTEAEAMMLWHMIINVKLVNVSFGYSPHCSEPGWFRVCYANMDDETVEALTR 428

QY 431 IRNEV---LQNKVVVSNKKHCW-HSNLRLSLKTRRFDIT-----NSPISPLPQSPMW 480

Db 429 INTFGKTKRDEMVKQK-----WQRNLQSFSSIRRFVHETIMSPHMMSPHSPIQSPVLV 484  
Qy 481 KAT 483  
111  
Db 485 KAT 487  
111  
RESULT 11  
T13019  
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) ACS-6 - Arabidopsis thaliana  
N:Alternate names: ACC synthase; protein F8L21.70  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 04-Feb-2000  
C:Accession: T13019  
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew  
submitted to the Protein Sequence Database, July 1999  
A:Reference number: 217587  
A:Accession: T13019  
A:Molecule type: DNA  
A:Residues: 1-495 <BEV>  
A:Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.70  
A:Experimental source: cultivar Columbia; BAC clone F8L21  
C:Genetics:  
A:Gene: ACS-6; ATSP:F8L21.70  
A:Map position: 4  
A:Introns: 60/3; 104/3; 158/2  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph  
F:280/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted  
Query Match 67.1%; Score 1716; DB 2; Length 495;  
Best Local Similarity 66.8%; Pred. No. 8.2e-129;  
Matches 322; Conservative 59; Mismatches 89; Indels 12; Gaps 3;  
Qy 11 LLSKMAIGDGHGESSPYDGCWKAYQDNFPHPTDNPNGVMQGLAENQLTSLDVEDWILNN 70  
Db 14 LLSKIASGDGHGENSEYFDGKWAYENPFHTDRPDGVIQMGLEAENLCGLDMRRKWLKH 73  
Qy 71 PEASICTPEGINDFRAINFQDYHGLAEFRNAVAFMARTGNRTTFDPDRIVMSGGATG 130  
Db 74 PEASICTSEGVNQFSDIAIFQDYHGLPEFRQAVAFMEKTRNKNKVPDPDRIVMSGGATG 133  
Qy 131 AHEVTAFLADGEAFLPIPYPGFDRDLRWRTGKLVPMCDSSNNFVLTKALEDAY 190  
Db 134 AHETVAFCLANPDGFLVPTPYPGFDRDLRWRTGVLNVPVTVCHSSNGFKITVEALEAAY 193  
Qy 191 EKAREDNIRVGLLTINPSNLPGTTMDRKTLETVVYFNEKRIHLVCDIEYAATVFSQPG 250  
Db 194 ENARKSNIPVKGLLTNPSNLPGTTMDRCKLSLVNFTNDKGIHLIADEIYAATVFGQSE 253  
Qy 251 FLSIAEILEDFTDIEDCNLHVIVYSLSKDMGFPQFRVGIYISNDVYVNCARKMSSFGL 310  
Db 254 FLSVAEVEEIED--CNRDLIHIVYSLSKDMGLPGLRGVIVSYNDRVVQIARKMSSFGL 311  
Qy 311 VSTQYQYLLASMLNDEPVERFLASAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370  
Db 312 VSSQTHLIATKMLSDPEFVDFEIRSKRLAARHAEITGLDGLGIGWLKAKAGLFLWMD 371  
Qy 371 LRQLLKKPTFDSSETELWKVIIHEVINYPGVSFFICTEPGFRVCYANWDMVAQIALQR 430  
Db 372 LRNLKTATFDSSETELWRVIVHQVLANYSPOGSPGFCHEPGRVFCVAFNADHKMTETALAR 431  
Qy 431 IRNFVLQNK-----VVYSNKKHCWHSNLRSLK--TRRFDDITMSPHSPLPQSPMW 480  
Db 432 INVFTSQLEETEKPMNATTHMAKKKKCNQSNLRLSFSDFTRRFDGFTSPHSFPVPSPLV 491  
Qy 481 KA 482  
11  
Db 492 RA 493

RESULT 12  
SI9677  
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 2 - tomato  
N:Alternate names: ACC synthase; S-adenosyl-L-methionine methylthioadenosine-lyase  
C:Species: Lycopersicon esculentum (tomato)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 03-Dec-1999  
C:Accession: SI9677; SI9678; S24358; B36201; A35516; A41985; B33103  
R:Rottmann, W.H.; Peter, G.F.; Oeller, P.W.; Keller, J.A.; Shen, N.F.; Nagy, B.P.; Ta  
J. Mol. Biol. 222, 937-961, 1991  
A:Title: 1-aminocyclopropane-1-carboxylate synthase in tomato is encoded by a multiple  
A:Reference number: SI9677; MUID:92106351  
A:Accession: SI9677  
A:Molecule type: DNA  
A:Residues: 1-485 <ROT>  
A:Cross-references: EMBL:X59139; NID:g19165; PIDN:CAA41855.1; PID:g19166  
A:Genetics: ACC  
A:Accession: SI9678  
A:Molecule type: mRNA  
A:Residues: 1-123,'V',125-485 <ROW>  
A:Cross-references: EMBL:X59145; NID:g19167; PIDN:CAA41856.1; PID:g19168  
R:Li, N.; Wiesman, Z.; Liu, D.; Mattoo, A.K.  
PES Lett. 306, 103-107, 1992  
A:Title: A functional tomato ACC synthase expressed in Escherichia coli demonstrates  
A:Reference number: S24358; MUID:92339529  
A:Accession: S24358  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 9-485 <LIN>  
A:Cross-references: EMBL:X62536; NID:g19163; PIDN:CAA44397.1; PID:g19164  
A:Experimental source: cv. Pix-Red  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991  
R:Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990  
A:Title: Characterization and sequencing of the active site of 1-aminocyclopropane-1-  
A:Reference number: A36201; MUID:91045911  
A:Accession: A36201  
A:Molecule type: protein  
A:Residues: 275-286 <YIP>  
R:Van Der Straeten, D.; Van Wiemeersch, L.; Goodman, H.M.; Van Montagu, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 4859-4863, 1990  
A:Title: Cloning and sequence of two different cDNAs encoding 1-aminocyclopropane-1-  
A:Reference number: A35516; MUID:90280476  
A:Accession: A35516  
A:Molecule type: mRNA  
A:Residues: 1-321,'P',323-398,'L',400-485 <VAN>  
A:Cross-references: GB:M34289; NID:g170363; PIDN:AAA81580.1; PID:g170364  
R:Yip, W.K.; Moore, T.; Yang, S.F.  
Proc. Natl. Acad. Sci. U.S.A. 89, 2475-2479, 1992  
A:Title: Differential accumulation of transcripts for four tomato 1-aminocyclopropane  
A:Reference number: A41985; MUID:92196141  
A:Accession: A41985  
A:Molecule type: mRNA  
A:Residues: 208-310 <YI2>  
A:Note: sequence extracted from NCBI backbone (NCBIN:88505, NCBIP:88522)  
C:Genetics: <ACC>  
A:Gene: ACC2  
A:Introns: 57/3; 100/3; 154/2  
C:Function:  
A:Description: catalyzes the conversion of S-adenosylmethionine to 1-aminocyclopropan  
A:Pathway: ethylene biosynthesis  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal pho  
F:278/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental  
Query Match 66.9%; Score 1713; DB 1; Length 485;  
Best Local Similarity 65.6%; Pred. No. 1.4e-128;  
Matches 319; Conservative 72; Mismatches 89; Indels 6; Gaps 4;  
Qy 1 MGFKAMDQTPLLSKMAIGDGHGESSPYDGCWKAYQDNFPHPTDNPNGVMQGLAENQLTS 60  
Db 1 MGFEAKTNSILSKLATNEEHGENSEPYDGCWKAYSDPDPHPLKNPNGVQMGLEAENQLCL 60





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 21, 2002, 02:08:10 ; Search time 66.98 Seconds  
(without alignments)  
1250.068 Million cell updates/sec

Title: US-09-763-957-2

Perfect score: 2559

Sequence: 1 MGRAMDQTPLLSKMAICDG.....DITMSPHSLPQSPMVKATN 484

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvrius:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2559	100.0	484	10 Q43858	Q43858 phaseolus a
2	2115.5	82.7	487	10 O22464	O22464 pisum sativ
3	1945	76.0	487	10 Q9MB64	Q9MB64 malus domes
4	1922	75.1	489	10 P93772	P93772 pelargonium
5	1913	74.8	487	10 Q9MB65	Q9MB65 malus domes
6	1881.5	73.5	481	10 Q9MB76	Q9MB76 populus eup
7	1876	73.3	490	10 Q9FEM2	Q9FEM2 cucumis mel
8	1874	73.2	490	10 Q9MB85	Q9MB85 cucumis mel
9	1873.5	73.2	483	10 Q9S711	Q9S711 citrus sine
10	1863.5	72.8	489	10 O82124	O82124 cucumis sat
11	1823	71.2	487	10 Q9ZRC8	Q9ZRC8 carica papa
12	1791.5	70.0	483	10 Q49904	Q49904 nicotiana t
13	1785.5	69.8	485	10 Q94116	Q94116 cucurbita m
14	1781.5	69.6	483	10 Q96580	Q96580 lycopersico
15	1781	69.6	482	10 O65328	O65328 nicotiana g
16	1776	69.4	484	10 O65210	O65210 nicotiana g

17	1771.5	69.2	483	10 Q9S853	Q9S853 lycopersico
18	1765.5	69.0	486	10 Q9FXS0	Q9FXS0 solanum tub
19	1764	68.9	484	10 Q9SC82	Q9SC82 nicotiana t
20	1762.5	68.9	486	10 Q9MB75	Q9MB75 populus eur
21	1755.5	68.6	485	10 Q9S854	Q9S854 lycopersico
22	1750.5	68.4	485	10 Q96579	Q96579 lycopersico
23	1747.5	68.3	477	10 P93235	P93235 lycopersico
24	1743.5	68.1	477	10 Q94GA2	Q94GA2 lycopersico
25	1740.5	68.0	477	10 Q9SAZ4	Q9SAZ4 lycopersico
26	1735.5	67.8	489	10 O49123	O49123 rumex palus
27	1732	67.7	486	10 O81636	O81636 musa acumin
28	1721	67.3	490	10 Q43813	Q43813 petunia hyb
29	1719.5	67.2	487	10 Q9SEJ9	Q9SEJ9 lupinus alb
30	1719.5	67.2	485	10 Q9SXN9	Q9SXN9 pyrus pyrif
31	1717.5	67.1	485	10 Q9XWJ6	Q9XWJ6 musa acumin
32	1716	67.0	495	10 Q9SUT3	Q9SUT3 arabidopsis
33	1714	67.0	486	10 Q9SLY6	Q9SLY6 musa acumin
34	1712	66.9	486	10 Q9SVT9	Q9SVT9 musa acumin
35	1711.5	66.9	492	10 Q9LRC1	Q9LRC1 prunus pers
36	1709.5	66.8	477	10 Q9SMH1	Q9SMH1 citrus sine
37	1701.5	66.5	488	10 O49819	O49819 carica papa
38	1701.5	66.5	489	10 O65209	O65209 nicotiana g
39	1700	66.4	477	10 P94005	P94005 lycopersico
40	1693.5	66.2	482	10 Q43810	Q43810 pelargonium
41	1674	65.4	486	10 O65841	O65841 musa acumin
42	1667	65.1	491	10 Q43747	Q43747 brassica ol
43	1652	64.6	486	10 O82719	O82719 arabidopsis
44	1651.5	64.5	493	10 Q9MB86	Q9MB86 cucumis mel
45	1648.5	64.4	459	10 O82679	O82679 citrus sine

#### ALIGNMENTS

RESULT 1

Q43858 ID Q43858 PRELIMINARY; PRT; 484 AA.  
AC Q43858;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE 1-AMINOCYCLOPROPANE 1-CARBOXYLATE SYNTHASE (EC 4.4.1.14).  
OS Phaseolus aureus (Mung bean) (Vigna radiata).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
OX NCBI\_TaxID=3916;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=RWILCZ, AND CV. BERKEN; TISSUE=ETIOLATED HYPOCOTYL;  
RX MEDLINE=93043033; PubMed=1421146;  
RA Botella J.R., Arteca J.M., Schlaghauser C.D., Arteca R.N.,  
RA Phillips A.T.;  
RT "Identification and characterization of a full-length cDNA encoding  
RT for an auxin-induced 1-aminocyclopropane-1-carboxylate synthase from  
RT etiolated mung bean hypocotyl segments and expression of its mRNA in  
RT response to indole-3-acetic acid.";  
RL Plant Mol. Biol. 20:425-436(1992).  
CC -|- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -|- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC  
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).  
CC -|- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
CC AMINOTRANSFERASES.  
DR EMBL; Z11613; CAA77688.1; -.  
DR HSSP; P37821; 1B8G.  
DR InterPro; IPR001176; ACC\_synthase.  
DR InterPro; IPR001511; Aminotran\_1.  
DR Pfam; PF00155; aminotran\_1\_2; 1.  
DR PRINTS; PR00753; ACCSYNTHASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1; 1.  
KW Lyase; Pyridoxal phosphate.  
SQ SEQUENCE 484 AA; 5646 MW; E55388B0F7F71478 CRC64;

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Query Match      100.0%; Score 2559; DB 10; Length 484;
Best Local Similarity 100.0%; Pred. No. 3.9e-195;
Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTS 60
   |||||
Db 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTS 60
   |||||

Qy 61 DLVEDWILNNEPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGNRTTFDPD 120
   |||||
Db 61 DLVEDWILNNEPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGNRTTFDPD 120
   |||||

Qy 121 RIVMSGGATGAHEVTAFCIADPGEAFLVPIPYPGFDRDLRWRTGVKLVPMVCDSSNNFV 180
   |||||
Db 121 RIVMSGGATGAHEVTAFCIADPGEAFLVPIPYPGFDRDLRWRTGVKLVPMVCDSSNNFV 180
   |||||

Qy 181 LTKEALDAYEKAREDNIRVKGILLITNPSNPLGTIMDRKTLRTVVVFINEKRIHLVCDDEI 240
   |||||
Db 181 LTKEALDAYEKAREDNIRVKGILLITNPSNPLGTIMDRKTLRTVVVFINEKRIHLVCDDEI 240
   |||||

Qy 241 YAAVTFSPQGFISIAEILEDTEICDRNLVHIVYVSLSKDMGFGFRVGIITYSYNDVAVN 300
   |||||
Db 241 YAAVTFSPQGFISIAEILEDTEICDRNLVHIVYVSLSKDMGFGFRVGIITYSYNDVAVN 300
   |||||

Qy 301 CARKMSSFGVLSTQTYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGGLAKVGIKCLQ 360
   |||||
Db 301 CARKMSSFGVLSTQTYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGGLAKVGIKCLQ 360
   |||||

Qy 361 SNAGLFVWMDLRQLLKPTFSETELWKVIIHEVKINSPGYSFHCTEPGFRVCYANMD 420
   |||||
Db 361 SNAGLFVWMDLRQLLKPTFSETELWKVIIHEVKINSPGYSFHCTEPGFRVCYANMD 420
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Qy 421 DMVQIALQRIIRNFVQLNKEVVSNNKHCWHSNLRSLSKTRRFDITMSPHSPLPQSPMV 480
   |||||
Db 421 DMVQIALQRIIRNFVQLNKEVVSNNKHCWHSNLRSLSKTRRFDITMSPHSPLPQSPMV 480
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Qy 481 KATN 484
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Db 481 KATN 484

RESULT 2
O22464 ID O22464 PRELIMINARY; PRT; 487 AA.
AC O22464;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
GN ACS2.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98340552; PubMed=9675901;
RA Peck S.C., Kende H.;
RT "A gene encoding 1-aminocyclopropane-1-carboxylate (ACC) synthase
RL produces two transcripts: elucidation of a conserved response.";
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99084749;
RA Peck S.C., Kende H.;
RT "Differential regulation of genes encoding 1-aminocyclopropane-1-
RL carboxylate (ACC) synthase in etiolated pea seedlings: effects of
RL indole-3-acetic acid, wounding, and ethylene.";
RL Plant Mol. Biol. 38:977-982(1998).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN MUSKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; AF016459; AAD04199.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA-TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 487 AA; 55116 MW; 8485B1DB38497634 CRC64;

Query Match      82.7%; Score 2115.5; DB 10; Length 487;
Best Local Similarity 81.1%; Pred. No. 7.2e-160;
Matches 394; Conservative 47; Mismatches 42; Indels 3; Gaps 2;

Qy 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFPHTDNPNGVMQGLAENQLTS 60
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Db 1 MGVMNLDPQLLSKLTAMGDGHEASSYFDGWKAYDKDPFHPKSPKHGVIQMGAEQLTA 60
   || ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 DLVEDWILNNEPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTGNRTTFDPD 120
   |||||
Db 61 DMVQNWIMNSPEASICTLEGVHNFKQMANFQDYHGLPEFRNAVAKFMSRTRGNRTTFDPE 120
   |||||

Qy 121 RIVMSGGATGAHEVTAFCIADPGEAFLVPIPYPGFDRDLRWRTGVKLVPMVCDSSNNFV 180
   |||||
Db 121 RIVMSGGATGAHEVTAFCIADPGEAFLVPTPYPGFDRDLRWRTGVKLVPTVCSSNNFK 180
   |||||

Qy 181 LTKEALDAYEKAREDNIRVKGILLITNPSNPLGTIMDRKTLRTVVVFINEKRIHLVCDDEI 240
   |||||
Db 181 LTQKALEAYEKAREDNIRVKGILLITNPSNPLGTVMDRNTLATVTFINEKRIHLISDEI 240
   |||||

Qy 241 YAAVTFSPQGFISIAEILEDTEICDRNLVHIVYVSLSKDMGFGFRVGIITYSYNDVAVN 300
   |||||
Db 241 YAAVTFSPHSFISIAEIIIEHDTEICDRNLVHIVYVSLSKDMGFGFRVGIITYSYNDVVD 300
   |||||

Qy 301 CARKMSSFGVLSTQTYLLASMLNDDFVERFLAESAKRLAQRFRVFTGGGLAKVGIKCLQ 360
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Db 301 CTRKMSSEGLVSTQTYLLAKMLSDDDFVEKEFLPESAKRLAORYRVFTGGGLKVGIKCLQ 360
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Qy 361 SNAGLFVWMDLRQLLKPTFSETELWKVIIHEVKINSPGYSFHCTEPGFRVCYANMD 420
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Db 361 SNGGLFVWMDLRGLLKNAFTFESEIELWRVIIHEVKINSPGYSFHCSPGFRVCYANMD 420
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Qy 421 DMVQIALQRIIRNFVQLNKEVVS--NKKHCWHSNLRSLSKTRRFDITMSPHSPLPQSP 477
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Db 421 DRDQVIALQIRISFVTQNNKEAMGSKNPKYWHNSNLRSLSKPRRFDITMSPHSPIPOS 480
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Qy 478 PMVKAT 483
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Db 481 PLVKAT 486

RESULT 3
Q9MB64 ID Q9MB64 PRELIMINARY; PRT; 487 AA.
AC Q9MB64;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
GN MDACS-5B.
OS Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids I; Rosales; Rosaceae; Maloideae; Malus.
RN NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
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RA Sunako T., Ishikawa R., Senda M., Akada S., Nilizeki M., Harada T.;  
RT "MADS-5A (Accession No. AB034992) and 5B (Accession No. AB034993),  
RT two wound-responsive genes encoding 1-aminocyclopropane-1-carboxylate  
RL Plant Physiol. 122:620-620(2000).";  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC  
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
CC AMINOTRANSFERASES.  
DR EMBL; AB034993; BAA92351.1; -.  
DR HSSP; P37821; 1B8G.  
DR InterPro; IPR001176; ACC\_synthase.  
DR Pfam; PF00155; aminotran\_1.  
DR PRINTS; PR00753; ACCSYNTHASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1.  
KW Pyridoxal phosphate.  
SQ SEQUENCE 487 AA; 54648 MW; D23B9FCB1C68794F CRC64;

Query Match 76.0%; Score 1945; DB 10; Length 487;  
Best Local Similarity 73.4%; Pred. No. 2.6e-146;  
Matches 359; Conservative 63; Mismatches 59; Indels 8; Gaps 3;

QY 1 MGFKANDQTPLLSKMAGDGHGESSYFDGKAYDQNPFPHTDNPNGVMQGLAENQLT 60  
DB 1 MGFTLSNQQLLSKATGNGHNSPYFDGKAYDSDPHTKPNNGVQMGLAENQMC 60

QY 61 DLVEDILNPEASICTPGINDFRAIANFDYHGLAEFRNAVAKFMARTGRNRTFPD 120  
DB 61 DLIQEWILNPEASICTAGVNEFKDIAFDYHGLPEFRNAVANFMGVRGNRTFAD 120

QY 121 RIVMSGGATGAHEVTAFCADPGAEFLVPIYPYPGFDRLDRLWRTGKLVPMCDSSN 180  
DB 121 RIVMSGGATGAHEMIAFCADPGAEFLVPIYPYPGFDRLDRLWRTGKLVPMCDSSN 180

QY 181 LKAELEDAEYAKARENIRVKGILLINPSNPLGTIMDRKTLRTVVSFNEKRIHLV 240  
DB 181 VTAALEAEYAKAQRANIRVKGILLINPSNPLGTILDRDRLTSLVTFINEKRIHLV 240

QY 241 YAATVFSQPGFTSIABILEDETIECDRLNLIHVIVSLSKDMGPGFRVGIYSYNDA 300  
DB 241 YAATVFSQPSFTSIABILEE--NIGCNRLNLIHVIVSLSKDMGPGFRVGIYSYNDA 298

QY 301 CARKMSFGLVSTQTOYLLASMLNDDEFERFLAESAKRLAQRFRVFTGGLAKVGIC 360  
DB 299 CARKMSFGLVSTQTOYLLASMLSDNEFVKRFTAQSAKRLKTRMRFTMGLAQVSTN 358

QY 361 SNAGLFWMDRLKLLKPPFSDSETELWKVIVHEVKINSPGYSFHCTEPGFRVVCYAN 420  
DB 359 SNGGLEFVMDRLRLLEKQTEFAEMVLRWIIHEVKINSPGYSFHCTEPGFRVVCAN 418

QY 421 DMAVOIALORIRNFVLONKEVVVSNKKH-CWHSNRLSLKTRREDD- ----ITMSPH 474  
DB 419 DKTMEVALTRITFVLQNKEAIVPRKSNRLWHSNRLSLKTRREDDTMMSPCMSPHT 478

QY 475 POSPMVKAT 483  
DB 479 POSPLYRAT 487

RESULT 4  
ID P93772 PRELIMINARY; PRT; 489 AA.  
AC P93772;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.  
GN GACS2.  
OS Pelargonium hortorum.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC Geraniales; Geraniales; Pelargonium.  
OX NCBI\_TaxID=4031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=88-51-10'; TISSUE=PISTIL;  
RX MEDLINE=97435971; PubMed=9290638;  
RA Clark D.G., Richards C., Hilloti Z., Lind-Iversen S., Brown K.;  
RT "Effect of pollination on accumulation of ACC synthase and ACC oxidase  
RT transcripts, ethylene production and flower petal abscission in  
RT geranium. (Pelargonium x hortorum L.H. Bailey).";  
RL Plant Mol. Biol. 34:855-865(1997).  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC  
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
CC AMINOTRANSFERASES.  
DR EMBL; U88971; AAB70885.1; -.  
DR HSSP; P37821; 1B8G.  
DR InterPro; IPR001176; ACC\_synthase.  
DR Pfam; PF00155; aminotran\_1.  
DR PRINTS; PR00753; ACCSYNTHASE.  
DR PROSITE; PS00105; AA\_TRANSFER\_CLASS\_1.  
KW Pyridoxal phosphate.  
SQ SEQUENCE 489 AA; 55086 MW; 48F71F64B22113D1 CRC64;

Query Match 75.1%; Score 1922; DB 10; Length 489;  
Best Local Similarity 73.3%; Pred. No. 1.8e-144;  
Matches 354; Conservative 68; Mismatches 53; Indels 8; Gaps 5;

QY 7 DQTPLLSKMAGDGHGESSYFDGKAYDQNPFPHTDNPNGVMQGLAENQLTSDLV 66  
DB 9 NQRTLLSKMATGDGHGESSYFDGKAYDNNPFLHTQNGVQMGLAENQSLFELIQ 68

QY 67 ILNPEASICTPGINDFRAIANFDYHGLAEFRNAVAKFMARTGRNRTFPDRIVMS 126  
DB 69 VLNQPASICTAQGLQEFKDTAIFQDYHGLPEFRNAVANFMGVRGNRTFPDRIVMS 128

QY 127 GATGAHEVTAFCADPGAEFLVPIYPYPGFDRLDRLWRTGKLVPMCDSSN 186  
DB 129 GATGAHEMIAFCADPGAEFLVPIYPYPGFDRLDRLWRTGKLVPMCDSSN 188

QY 187 EDAYEKARENIRVKGILLINPSNPLGTIMDRKTLRTVVSFNEKRIHLVDEIYAAT 246  
DB 189 EAYERAQENIRVKGILLINPSNPLGTILDRDRLTSLVTFINEKRIHLVDEIYAAT 248

QY 247 SQPGFTSIABILEDETIECDRLNLIHVIVSLSKDMGPGFRVGIYSYNDAVNCAR 306  
DB 249 SQPAFVSIAEIVQOE--NVSCNRLNLIHVIVSLSKDMGPGFRVGIYSYNDAVNCAR 307

QY 307 SFGVSTQTOYLLASMLNDDEFERFLAESAKRLAQRFRVFTGGLAKVGICL 366  
DB 308 SFGVSTQTOYLLASMLSDNEFVKRFTAQSAKRLKTRMRFTMGLAQVSTN 367

QY 367 VMDRLKLLKPPFSDSETELWKVIVHEVKINSPGYSFHCTEPGFRVVCYANMD 426  
DB 368 IWDRLKLLKPPFSDSETELWKVIVHEVKINSPGYSFHCTEPGFRVVCYANMD 427

QY 427 ALQIRNFVLONKEVVV--SNKKHCHWSNRLSLKTRREDDIT-- --MSPHSPL 480  
DB 428 ALRRITFALQNKAAVLPALPAKQCNLGRSLSRFRDFTMSPHSPL--QSPLV 486

QY 481 KAT 483  
DB 487 RAT 489

RESULT 5  
Q9MB65

ID	Q9MB55	PRELIMINARY;	PRT:	487 AA.
AC	Q9MB65;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.			
GN	MDACS-5A.			
OS	Malus domestica (Apple) (Malus sylvestris).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;			
OC	eurosid I; Rosales; Rosaceae; Maloideae; Malus.			
OX	NCBI_TaxID=3750;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RP	Sunako T., Ishikawa R., Senda M., Akada S., Niizeki M., Harada T.;			
RP	"MdACS-5A (Accession No. AB034992) and 5B (Accession No. AB034993),			
RT	two wound-responsive genes encoding 1-aminocyclopropane-1-carboxylate			
RT	synthase in apple. (PGR00-030).";			
RL	Plant Physiol. 122:620-620(2000).			
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).			
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC			
CC	ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT			
CC	AMINOTRANSFERASES.			
DR	EMBL; AB034992; BAA92350.1; -.			
DR	HSSP; P37821; 1B8G.			
DR	InterPro; IPR001176; ACC synthase.			
DR	InterPro; IPR001511; Aminotran_1.			
DR	Pfam; PF00155; aminotran_1.2; 1.			
DR	PRINTS; PR00753; ACCSYNTHASE.			
DR	PROSITE; PS00105; AA_TRANSFASER.			
DR	Pyridoxal phosphate.			
SW	SEQUENCE 487 AA, 54876 MW; 3E9899EF2EBA73368 CRC64:			

[illegible]

Db	479	QPSPLVRAT	487	: :
RESULT	6			
Q9MB76				
ID	Q9MB76	PRELIMINARY;	PRT:	481 AA.
AC	Q9MB76;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2001 (TREMBLrel. 19, Last annotation update)			
DE	1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.			
GN	PEACS-1.			
OS	Populus euphratica.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid I; Malpighiales; Salicaceae; Populus.			
OX	NCBI_TaxID=75702;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-CV. I-45/51;			
RA	Koch J.R., Minocha R., Nakajima N., Yasutani I., Saiji H., Rebbeck J.,			
RA	Davis K.R.;			
RT	"Induction of ethylene and putrescine by ozone: Comparison of an			
RT	ozone-sensitive and an ozone-tolerant hybrid popular clone.";			
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
CC	-1- CFACTOIR (PYRIDOXAL PHOSPHATE (BY SIMILARITY).			
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).			
CC	-1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC			
CC	ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT			
CC	AMINOTRANSFERASES.			
DR	EMBL; AB033502; BAA94599.1; -.			
DR	HSSP; P37821; 1B8G.			
DR	InterPro; IPR001176; ACC synthase.			
DR	InterPro; IPR001511; Aminotran.1.			
DR	Pfam; PF00155; aminotran.1.2; 1.			
DR	PRINTS; PR00753; ACCSYNTHASE.			
DR	PROSITE; PS00105; AA_TRANSF.			
DR	Pyridoxal phosphate.			
SK	SEQUENCE 481 AA; 54754 MW; DFD45B87248DB0B CRC64;			

Query Match	73.5%	Score 1881.5	DB 10	Length 481
Best Local Similarity	73.5%	Pred. No. 2.9e-141		
Matches 349	Conservative 58	Mismatches 65	Indels 3	Gaps 2

  

Qy	11	LLSKWATGDGHGESSPYFDGHWKAYDQNPFPHTDPNPGVMQGLAENQITSDLVEDWTLNN	70
Db	9	LLSRIASDGHGESSPYFDGHWKAYSDSPHPTDPNPGVIQMGLEAGLCTFLDIODWLKKN	68
Qy	71	PEASICTEGINDPRAJANFQDYHGLAEFRNAVAKFNARTGRITFDPDRIVMSGGATG	130
Db	69	PKASICSPEGLNEFRETATFQDYHGLAEFRNAVANFMEKVRGNRVTFDPDRIVMSGGATG	128
Qy	131	AHEVTAFLCADPGAEAFVLPYIPYPGFDRDLRWRTGVKLVPMVCDSSNNEVLTKALEADAY	190
Db	129	AHETIAFLCADPGAEAFVLPYIPYPGFDRDLRWRTGVKLLIPVDSOSSNNMVTREALENAY	188
Qy	191	EKAREDNRVKGLLITNPSNPLGTIMDRKRLTRTVVSINERKRIHLVDEIYAAVTFVSQPG	250
Db	189	EKAOLDNRVKGLLITNPSNPLGTILDRETLRSLVRFINEKNIHLVGEIYAAVTFVSQPD	248
Qy	251	FISTAELLIEDTLECDORNVLHVIYSLSKDMPGPFVRVGIYYSNDVAVNCARKWSSFGL	310
Db	249	FISVRIQLQE--DIECNLDLHVIIYSLSKDMPGFLGRVGIYYSNDVAVNCARKWSSFGL	306
Qy	311	VSTQTYLLASMLNDDEVERFLAESAKRLAQRFRVFTGGKLVAKYIKCLQ--SNAGLEFVWM	369
Db	307	VSTQTYLLASMLSDNEFVEMFIESKRRLAARYVETFRGLDQVIGICLTKTSNAGLEFLWM	366
Qy	370	DLROLLKKPTFDSTELWKVIIHEVKINVSFGYSFHCTEPGCFWRVCYVANDMNAVIALQ	429



Db	367	DLSKLLKQQTFKAEMLWRIYIHEVKLVNVSPOCSFHCLKPGWFRVCFVAMDMDETQVALS	426
Qy	430	RIRNFVLQNEVVVSNKKHWSNLRSLKTRRFDITMSPHSPLQSPQPMVKATN	484
Db	427	RKTFYVKNKEADTKSRKNLRWQSLKLLNSPRIYDDFINSPHSPIQSPPIVARN	481
RESULT	7		
Q9FEM2			
ID	Q9FEM2	PRELIMINARY; PRT; 490 AA.	
AC	Q9FEM2		
DT	01-MAR-2001 (T-EMBLrel. 16, Created)		
DT	01-MAR-2001 (T-EMBLrel. 16, Last sequence update)		
DT	01-DEC-2001 (T-EMBLrel. 19, Last annotation update)		
DE	1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.		
GN	CME-ACS2 (ME-ACS2).		
OS	Cucumis melo (Muskmelon).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid I; Cucurbitales; Cucurbitaceae; Cucumis.		
OX	NCBI_TaxID=3656;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPRAIN-AMS;		
RC	PUBMED-11074269;		
RA	Ishiki Y., Oda A., Yaegashi Y., Orihara Y., Arai T., Hirabayashi T.,		
RA	Nakagawa H., Sato T.;		
RT	"Cloning of an auxin-responsive 1-aminocyclopropane-1-carboxylate		
RT	synthase gene (CME-ACS2) from melon and the expression of ACS genes in		
RT	etiolated melon seedlings and melon fruits.,"		
RL	Plant Sci. 159:173-181(2000).		
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).		
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC		
CC	ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT		
CC	AMINOTRANSFERASES.		
DR	EMBL; D86242; BAB18464.1; -.		
DR	HSSP; P37821; 1B8G.		
DR	InterPro; IPR001176; ACC_synthase.		
DR	InterPro; IPR001511; AminoTran_1.		
DR	Pfam; PF00155; aminotran_1_2; 1.		
DR	PRINTS; PR00753; ACCSYNTHASE.		
DR	PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.		
KW	Pyridoxal phosphate.		
SQ	SEQUENCE 490 AA; 54904 MW; 95754805F958C8FB CRC64;		
Query Match	73.3%; Score 1876; DB 10; Length 490;		
Best Local Similarity	72.9%; Pred. No. 8e-141;		
Matches	347; Conservative 62; Mismatches 63; Indels 4; Gaps		
Qy	11	LLSKMATGDGHGSSSYFDGWKAYDONPHPTDNPNGVMQGLAENQITSLDVEDILNN	70
Db	15	VLSKLAGNGHGSDSYFDGWKAYSDPDPHPITINPRGVIQMGLEAENQLSFEEVKKWKN	74
Qy	71	PEASITCEGINFRAIANFDYVHGLAEFRNAVAFKMGRTNRTTFDPRIVMSGGAT	130
Db	75	PQASICSVEGIDFEKDIAFDQYHGLPERFNNAVAFMGKVRGRVKFDDPRVMSGGAT	134
Qy	131	AHEVTAFLADPGAEFLVPIPYPGFDRDLRWRGTGKLVPMVCDSSNNFNVLTKALEDAY	190
Db	135	AHETMAFLADPGAEFLVPPYPPGDFDRDLRWRGTGVEIYPVKCESSNNFKLTREALETAY	194
Qy	191	EKAREDNIKVGILLINPSNPLGTIMDRKLTFTVVSFNEKRIHLVCDIEIYAATVFSQP	250
Db	195	EAEKSNIRIKGILLINPSNPLGTIVYDQRTLETATVSFNEKNIHLVCDIEIYAATVFAEP	254
Qy	251	FISIAETLEDETIEDCRNLVHVTVSLSKDMGFCPGFRVGIIVSYNDAVVNCARKMSSFGL	310
Db	255	FISISEIVNNDDVDCRNLHVTVSLSKDMGFCPGFRVGIIVSYNDAVVNCARKMSSFGL	314
Qy	311	VSTQTOYLLASMLINDFEVERFLAESAKRLAQRFVFTGGLAKVGIKICQSNAGLFWMD	370

Db	315	VSSQTYLIASMLSDDDVFDVDFNFLAGSAEKIHAVRRNFTKGLAQVGIGYLGSGGLFAMD	374
Qy	371	LROLLKKPTDSETELMKWIIHEVKINSPGVSHFCHEPGRVVCYANMDDMAVOIALQR	430
Db	375	LRHLKKETLEAEMALKVIINEVKUNVSPGSHFCHEPGRVFCFANMDDSDTMDISITR	434
Qy	431	IRNFVLQNKQEVV--VSNKKHCW-HSNLRISLKTRRFDDITMSPHSPLPQSPMKAT	483
Db	435	IRNFVLQNKQEVVTKVKQKCEKQWSSLELRSSRLIEDI-MSPHSPLPQSPMLRAT	489
RESULT	8		
Q9MB85		PRELIMINARY; PRT; 490 AA.	
OC	Q9MB85;		
DT	01-OCT-2000 (Tremblrel. 15, Created)		
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)		
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE	1-AMINOACYCLOPROPANE-1-CARBOXYLATE SYNTHASE.		
GN	CME-ACS2.		
OS	Cucumis melo (Muskmelon).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.		
ON	NCBI_TaxID=3656;		
RX	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-CV. ANDES;		
RA	Shiomi S., Yamamoto M., Inaba A.;		
RT	"Structural characterization of ACC synthase gene from melon and		
RT	cucumber";		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
CC	-1- COPAFOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).		
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC		
CC	ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT		
CC	AMINOTRANSFERASES.		
DR	EMBL; AB032936; BAA93713.1; -.		
DR	HSSP; P37821; I88G.		
DR	InterPro; IPR001176; ACC_synthase.		
DR	InterPro; IPR001511; Aminotran_1.		
DR	Pfam; PF00155; aminotran_1_2; 1.		
DR	PRINTS; PR00753; ACCSYNTHASE.		
DR	PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.		
KW	Pyridoxal phosphate.		
Qy	SEQUENCE 490 AA; 54932 MW; 63B4732473E3F36E CRC64;		
Query Match	73.2%;	Score 1874;	DB 10; Length 490;
Best Local Similarity	72.9%;	Pred. No. 1.2e-140;	
Matches 34;	Conservative 61;	Mismatches 64;	Indels 4; Gaps
Qy	11	LLSKMAIGDGHGESSPYDGWKAYDQNPHTDPNGVMQGLAENQLTSDLVEDWILNN	70
Db	15	VLSKLAGNGHGSDSYDGWKAYDSDPPHPIINPRGVIQMGLAENQLSFEEVEMKNN	74
Qy	71	PEASICTEPIINDPRATANTQDHYGLAEFRNAVAKEMATRGNRITFDPRIVMSGGATG	130
Db	75	PQASICEVEGIDEFKDAIFQDYHGLPEFRNAVANFMGVKRVGRVKKVDPDRVVMGGATG	134
Qy	131	AHEVTAECIADPGAEFLVPIPYPGDFDRDLRWETGKLVPMVCDSSNNFVLTKAELEAY	190
Db	135	AHETMAFCIADPGAEFLVPIPYPGDFDRDLRWETGVEIVPVKCESSNNFKLTREALETAY	194
Qy	191	EKAREDNRVKGLLITNPSNPLGTIMDRKTLRWTSFINEKRIHLVCDIEYAAATVFSOPG	250
Db	195	EAEKSNIRIKGLITNPSNPLGTIVYDQRLTAVSFINEKRIHLVCDIEYAAATVFSPPG	254
Qy	251	FISTAIELEDFTDIECDRNLIHVIVSLSKDMPGPGFRVGIISYNDVAVNCARKMSSFGL	310
Db	255	FISTISEVDNNNDVECDRNLIHVIVSLSKDMPGPGFRVGIISYNDVAVNCARKMSSFGL	314



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QY 71 PEASICTPEGINDPRAIANFQDYHGLAEPRNAVAKFWARTGRNRTITFDDPDRIVMSGGATG 130
Db 75 PRASICSVEGIDEIDFKDIAIFQDYHGLPEFRNAVANFMKVRGRVRFDPDRVVMSSGGATG 134
QY 131 AHEVTAFLADPGEAFVLPIPPYPYGGFDRDLRWRTGKVLVPMCDSSNNFVLTKEALEDAY 190
Db 135 AHEVTAFLADPGEAFVLPIPPYPYGGFDRDLRWRTGKVLVPMCDSSNNFVLTKEALEDAY 194
QY 191 EKAREDIRVKGILLITNPSNPLGTIMDRKTLRTVVSFNEKRIHLVDEIYAATVFSQPG 250
Db 195 EEAQSNIKIKGLLITNPSNPLGTIVDROPLETAVSFINEKRIHLVDEIYAATVFAEPG 254
QY 251 FISIAETLEDTECDRNLVHVIYSLSKDMGFGFRVGIYIYNDVAVNCARKMSFGL 310
Db 255 FISISEVI-DNSDIECDRNLVHVIYSLSKDMGFGFRVGIYIYNDVAVNCARKMSFGL 313
QY 311 VSTQTYLLASMLNDDFEVERFLAESAKRLAQRFRVFTGGTGLAKVGIKCLQSNAGLFWMD 370
Db 314 VSSQTYLLASMLNDDFVDFNLAGSAEKLAARHNFETKGLAQVGIKCLQSNAGLFWMD 373
QY 371 LROLLKPTFDSFTELWKVIIHEVKINVSFGYFHCTEPGWFRVYCYANMDDMAVIALQR 430
Db 374 LRLLKPTFDSFTELWKVIIHEVKINVSFGYFHCSEPGWFRVYCYANMDDMAVIALQR 433
QY 431 IRNFVLQNEV--VSNKKHCW--HSNLRSLKTRRFDITMSPHSPLPQSPMVKAT 483
Db 434 IRNFVLQNEVTVKKQKFCWQSSLESLRRLJEDI-MSPHSPLPQSPMHRAT 488

RESULT 11
QY2RC8 PRELIMINARY; PRT; 487 AA.
AC QY2RC8
DT 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE ACC SYNTHASE.
OS Carica papaya (Papaya).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Caricaceae; Carica.
OX NCBI_TaxID=3649;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUNSET; TISSUE=30% YELLOW FRUIT;
RA Neupane K.R., Mukitira U.T., Stiles J.I.;
RT "Cloning of Fruit-specific ACC Synthase and ACC Oxidase cDNAs From
RT Papaya (Carica papaya L.) and Their Expression During Fruit
RT Ripening.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; U68216; AAC98809.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran.1.
DR Pfam; PF00155; aminotran.1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 487 AA; 55059 MW; 571398012223DA35 CRC64;

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Query Match 71.2%; Score 1823; DB 10; Length 487;
Best Local Similarity 70.9%; Pred. No. 1.3e-136;
Matches 339; Conservative 65; Mismatches 66; Indels 8; Gaps 3;

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QY 11 LLSKMAIGDGHGESSPYFDGKAYDQNPFPHTDNPNGVQMGLAENQLTSDLVEDWILNN 70

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Db 10 LLSKIATSNHGDESPYFDGKAYDSDPFPHTQNPGEVQMGLEAENQLCFNLHIEWLLKN 69
QY 71 PEASICTPEGINDPRAIANFQDYHGLAEPRNAVAKFWARTGRNRTITFDDPDRIVMSGGATG 130
Db 70 PEASICTQAAGAEPRDIAIFQDYHGLAEPRNAVAKFWARTGRNRTITFDDPDRIVMSGGATG 129
QY 131 AHEVTAFLADPGEAFVLPIPPYPYGGFDRDLRWRTGKVLVPMCDSSNNFVLTKEALEDAY 190
Db 130 AHEVTAFLADPGEAFVLPIPPYPYGGFDRDLRWRTGKVLVPMCDSSNNFVLTKEALEDAY 189
QY 191 EKAREDIRVKGILLITNPSNPLGTIMDRKTLRTVVSFNEKRIHLVDEIYAATVFSQPG 250
Db 190 ETQAEADIKVKGILLIPNPSNPLGTITKDLTLEALVTNHNKRIHLVDEIYAATVFSQPE 249
QY 251 FISIAETLEDTECDRNLVHVIYSLSKDMGFGFRVGIYIYNDVAVNCARKMSFGL 310
Db 250 FTSIAETIE-EDKICCNRLDIIHIIYSLSKDMGFGFRVGIYIYNDVAVNCARKMSFGL 308
QY 311 VSTQTYLLASMLNDDFEVERFLAESAKRLAQRFRVFTGGTGLAKVGIKCLQSNAGLFWMD 370
Db 309 VSSQTYLLASMLNDDFEVDFQFIVESKRKLAMRHSFTQRLAQVGIKCLQSNAGLFWMD 368
QY 371 LROLLKPTFDSFTELWKVIIHEVKINVSFGYFHCTEPGWFRVYCYANMDDMAVIALQR 430
Db 369 LRLLKPTFDSFTELWKVIIHEVKINVSFGYFHCSEPGWFRVYCYANMDDMAVIALQR 428
QY 431 IRNFVLQNEVYVSNKKHCWHSNLRSLKTRRFDIT-----MSPHSPLPQSPMVK 482
Db 429 IKTFMLQHKEMVPPKKLCWQTSURLSFSS-RYEDINETPGSPHSPHPIQSPPLVRA 485

RESULT 12
QY2RC8 PRELIMINARY; PRT; 483 AA.
AC QY2RC8
DT 01-JUN-1998 (TREMREL. 06, Created)
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE ACC SYNTHASE.
GN ACCS2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Weterings K., Pezzotti M., Cornelissen M., Mariani C.;
RT "Pollination induced ACC-synthase and ACC-oxidase expression.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; X98492; CAA67118.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran.1.
DR Pfam; PF00155; aminotran.1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 483 AA; 54636 MW; C32E7AA38FC2DF0F CRC64;

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Query Match 70.0%; Score 1791.5; DB 10; Length 483;
Best Local Similarity 68.1%; Pred. No. 4.1e-134;
Matches 329; Conservative 79; Mismatches 72; Indels 3; Gaps 3;

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QY 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGKAYDQNPFPHTDNPNGVQMGLAENQLT 60

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Db 1 MGFISSIDNELLSKVATNNGHGENSAYFDGKAYEIDPFHPTQNSDGVQIOMGLAENQLCF 60
Qy 61 DLVEDWILNPNPEASTCTPEGINDFRAINFODYHCLAEFRNAVAFKEMARTGNRTITDPD 120
Db 61 DLQWVKNPNKASICTAEGSQDFADIAIYQDYHGLPEFRSAVARFMKVRGDRITFEPE 120
Qy 121 RIVMSGGATGAHEVTAFCIADPGEAFLVPIPIYPGDFDRDLRWRTGKLVPMCDSSNNFV 180
Db 121 RIVMSGGATGAHELLAFCLADPGEAFLVPTPYPGDFDRDLRWRTGVLFPVVCSSNNFK 180
Qy 181 LTKEALDAYEKARDNTRVGLLITNPSNPLGTIMDRKTLRTVVVSFINEKRIHLVCDDEI 240
Db 181 VTKEALAYQAQESNITVTRGLLNNPSNPLGTILDRTELKTVRFINEKRIHLVCDDEI 240
Qy 241 YAAVFSOPGFIETAEILEDETCDRLNHLVIVYSLSKDMGFCGFRVGIIVSYNDVAVN 300
Db 241 YAAITFNKPFDISISEVIMEE--DVECDRLNHLVIVYSLSKDGLGFGFRVGIIVSYNDVAVN 299
Qy 301 CARKNSSGLVSTOTQYLLASMLNDEFERFLAESAKRLAQRFRVFTGGLAKVGIKICQ 360
Db 300 CARKNSSGLVSTOTQYLLASMLNDEFERFLAESAKRLAQRFRVFTGGLAKVGIKICQ 360
Qy 361 SNAGLFVMDLRQLKKPTFSETELKVIIEHVKINVPYSGYSFCHCTEPGFRVVCYANMD 420
Db 360 SNAGLFVMDLRQLKKPTFSETELKVIIEHVKINVPYSGYSFCHCTEPGFRVVCYANMD 420
Qy 421 DMVQIALQRIRNFVLQNKVVSNNK--HCWHSNLRSLKTRRREDDITMSPHPLQSPQSM 479
Db 420 DETMRALRRIRNFVQIRKGTGGVKKLQCRSKLEISLFRKLDFFMNSPHSPM--SSPL 478
Qy 480 VKA 482
Db 479 VQA 481

RESULT 13
Q941I16 PRELIMINARY; PRT; 485 AA.
AC Q941I16;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE ACC SYNTHASE.
GN CM-ACS3.
OS Cucurbita maxima (Pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3661;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe T., Fujita H., Sakai S.;
RT *Effects of jasmonic acid and ethylene on the expression of three
RT genes for wound-inducible 1-aminocyclopropane-1-carboxylate synthase
RT in winter squash (Cucurbita maxima).;
RL Plant Sci. 161:67-75(2001).
DR EMBL; AB038559; BAB47124.1; -.
SQ SEQUENCE 485 AA; 54426 MW; 621598080D4EE9F3 CRC64;
```

```
Query Match 69.8%; Score 1785.5; DB 10; Length 485;
Best Local Similarity 70.0%; Pred. No. 1.2e-133;
Matches 334; Conservative 67; Mismatches 69; Indels 7; Gaps 5;

Qy 11 LLSKWAIGDGHGESSPYDGNKAYDONPHTDNPNGYMWQGLAENQLTSDLVEDWILNN 70
Db 11 LLSKLAUNGHGEDSPYDGNKAYDIDPFHPTMNPGRVQIOMGLAENQLSEFEVDWIKNN 70
Qy 71 PEASICTEGINDFRANFQDYHGLAEFRNAVAFKEMARTGNRTITDPDRIVMSGGATG 130
Db 71 POASICSVEGLDFKDIADFQDYHGLPEFRNWRILWKGVRGDRVKFDPDRVMSGGATG 130
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Qy 131 AHEVTAFCIADPGEAFLVPIPIYPGDFDRDLRWRTGKLVPMCDSSNNFVLTKAEALDAY 190
Db 131 AHEVTAFCIADPGEAFLVPIPIYPGDFDRDLRWRTGKLVPMCDSSNNFVLTKAEALDAY 190
Qy 191 EKARDNTRVGLLITNPSNPLGTIMDRKTLRTVVVSFINEKRIHLVCDDEIYAATVFSQPG 250
Db 191 EKAQESNIKIKGLITNPSNPLGTVCROTLETAVAFINQKKIHLVCDDEIYAATVTEPG 250
Qy 251 FTSIAEILEDFTDIEDRNLHVIYSLSKDMGFCGFRVGIIVSYNDVAVNCARKSSSFL 310
Db 251 FTSISEVLENDT--KCDNLHVIYSLSKDMGFCGFRVGIIVSYNDVAVNCARKSSSFL 308
Qy 311 VSTQYLLASMLNDEFERFLAESAKRLAQRFRVFTGGLAKVGIKICQSNAGLFVMD 370
Db 309 VSSQYLLASMLNDEFERFLAESAKRLAQRFRVFTGGLAKVGIKICQSNAGLFVMD 368
Qy 371 LRQLKKPTFSETELKVIIEHVKINVPYSGYSFCHCTEPGFRVVCYANMDMAVOIALQ 429
Db 369 LRHLLEKTELEAMALRWRIINDVKAECVAGVYVFFLLGSPGFRVVCYANMDTMEISIT 428
Qy 430 RIRNFVLQNKV--VSNKKHCW--HSNLRSLKTRRREDDITMSPHPLQSPQSMVKAT 483
Db 429 RIRNFVLQNKVTTKIKKQKFCROSSLELRSSRLEDI--MSHSPPLQSPMLRAT 484

RESULT 14
Q96580 PRELIMINARY; PRT; 483 AA.
AC Q96580;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE (EC 4.4.1.14) (ACC
DE SYNTHASE).
GN LE-ACSIB.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC Oono Y., Nguyen M.D., Hennig L., Yu G., Rottman W.H., Campbell A.D.,
RA Lincoln J.E., Theologis A.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 209-311 FROM N.A.
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE = 1-
CC AMINOCYCLOPROPANE-1-CARBOXYLATE + METHYLTHIOADENOSINE.
CC -1- COPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; U72390; AAB17279.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1.2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Lyase; Pyridoxal phosphate.
FT VARIANT 43 43 P -> L.
FT VARIANT 139 139 F -> L.
SQ SEQUENCE 483 AA; 54547 MW; 55681096DD7DC2 CRC64;
```

Query Match

69.6%; Score 1781.5; DB 10; Length 483;

Best Local Similarity 69.1%; Pred. No. 2.6e-133;  
Matches 327; Conservative 76; Mismatches 65; Indels 5; Gaps 3;

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QY 11 LLSKMAIGDHGSSYFDGKAYDQNPFPHTDNPNGVMQGLAENQLTS 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 13 LLSKIATNDHGSNSYFDGKAYANNPFPHTDNPNGVMQGLAENQLCF 72
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 71 PEASICTPEGINDFRATANFODYHGLAEFRNAVAKEMARTGRNRTTDPD 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 73 PKASICTVEGAENFQDIAIFQDHYHGLPEPQAVARMEKVRGRVTFDPNRI 132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 131 AHEVTAFLADPGAEFLVPTYPYGFEDRDLRWRTGKLVPMCDSSNNFVLTKE 190
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 133 AHEMLAFCLADPGAEFLVPTYPYGFEDRDLRWRTGKLVPMCDSSNNFV 192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 191 EKAREDNIRVKGLLITNPSPNLTGIMDRKTLRTVVSFINEKRIHLVCD 250
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 193 ERAQSNIRKIGLLINNPSPNLTGIMDRKTLRTVVSFINEKRIHLVCD 252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 251 FISIAELEDETDIECDRLNHLVIVSYLSKDMGFPGRVGIYSYNDVAVNC 310
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 253 FISVSEVEM--TECNTDLIHIVSYLSKDLGPPGRVGIYSYNDVAVNC 310
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 311 VSTQTOYLLASMLNDEFEVERFLAESAKRLAQRFTVTGGLAKVGIKCLQ 370
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 VSTQTOYLLASMLNDEFEVERFLAESAKRLAQRFTVTGGLAKVGIKCLQ 370
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 371 LROLLKPTFDSDELWKVITHEVKINVSFGYSHCTEPGFRVCYANMDMAV 430
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 371 LRLLKEATFDGELWRLIINEVKLVNPGSCSFHCEPGRVCFANMDMTRIA 430
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 431 IRNFVLQNEV--VSNKKHCWHSNLRSLKTRRFDITMSPHSPVQSPVK 481
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 431 IRNFVLQNEV--VSNKKHCWHSNLRSLKTRRFDITMSPHSPVQSPVK 482
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 15

```
O65328 PRELIMINARY; PRT; 482 AA.
AC O65328;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ACC SYNTHASE.
OS Nicotiana glutinosa (Tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=35889;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee Y.K., Lee S.H.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
CC -1- ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; AF061605; AAC15777.1; -.
DR HSSP; P37821; 1B8G.
DR InterPro; IPR001176; ACC_synthase.
DR InterPro; IPR001511; Aminotran_1.
DR Pfam; PF00155; aminotran_1_2; 1.
DR PRINTS; PR00753; ACCSYNTHASE.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
KW Pyridoxal phosphate.
SQ SEQUENCE 482 AA; 54617 MW; E556CE42C84D860B CRC64;
```

Query Match 59.6%; Score 1781; DB 10; Length 482;  
Best Local Similarity 68.6%; Pred. No. 2.8e-133;  
Matches 332; Conservative 74; Mismatches 72; Indels 6; Gaps 5;

```
QY 1 MGFKAMDQTPLLSKMAIGDHGSSYFDGKAYDQNPFPHTDNPNGVMQGLAENQLTS 60
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGFISGKN-KLLSKIAATSDHGSENSAYFDGKAYENDPFLHTQNPNGVIOGMLAENQLCF 59
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 DLVEDWILNPEASICTPEGINDFRATANFODYHGLAEFRNAVAKEMARTGRNRTTDPD 120
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 DLIQEVVNNPKASICTAEGNQDENDTAIFQDYHGLREFRKAVERMEKVRGDKVTFDDP 119
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 RIVMSGGATGAHEVTAFLADPGAEFLVPTYPYGFEDRDLRWRTGKLVPMCDSSNNFV 180
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 HIVMSGGATGAHEVTAFLADPGAEFLVPTYPYGFEDRDLRWRTGKLVPMCDSSNNFV 179
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 LTREALEDAYEKAREDNIRVKGLLITNPSPNLTGIMDRKTLRTVVSFINEKRIHLVCD 240
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 ITREALEDAYEKAREDNIRVKGLLITNPSPNLTGIMDRKTLRTVVSFINEKRIHLVCD 239
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 YAAVFSQPGFISIAELEDETDIECDRLNHLVIVSYLSKDMGFPGRVGIYSYNDVAVN 300
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 240 YAAVFSQPGFISIAELEDETDIECDRLNHLVIVSYLSKDMGFPGRVGIYSYNDVAVN 297
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 CARMKSSFGVLVSTQTOYLLASMLNDEFEVERFLAESAKRLAQRFTVTGGLAKVGIKCLQ 360
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 298 CARMKSSFGVLVSTQTOYLLASMLNDEFEVERFLAESAKRLAQRFTVTGGLAKVGIKCLQ 357
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 361 SNAGLFWMDLRQLLKPTFDSDELWKVITHEVKINVSFGYSHCTEPGFRVCYANMD 420
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 SNSGLFWMDLRQLLKPTFDSDELWKVITHEVKINVSFGYSHCTEPGFRVCYANMD 417
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 421 DMVQIATLQIRNFVLQNEV--VSNKKHCWHSNLR-LSLKTRRFDITMSPHSPVQSP 478
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 DETMRVALRIKHVFLQKGLIEVATKKQRRRRKRREISLSFRLLDDPMNSPHSPW-SSP 476
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 479 MVKA 482
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 477 MVQA 480
    ||| : : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: August 21, 2002, 02:11:26  
Job time: 196 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 00:26:04 ; Search time 3456.34 Seconds  
(without alignments)  
9660.932 Million cell updates/sec

Title: US-09-763-957-3  
Perfect score: 2474  
Sequence: 1 ttacagatacacagaatcag.....taaccacatacacacatatgg 2474

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries .

Database :

- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estmu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_htc.\*
- 9: gb\_estl.\*
- 10: gb\_est2.\*
- 11: gb\_htc.\*
- 12: gb\_gss.\*
- 13: em\_gss\_hum.\*
- 14: em\_gss\_inv.\*
- 15: em\_gss\_pln.\*
- 16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	132	5.3	1101	12	CNS00EVL	AL069706 Drosophil
2	130.6	5.3	1101	12	CNS00EVL	AL069706 Drosophil
3	122.2	4.9	1152	10	BG309087	BG309087 HVMSEC000
4	121	4.9	1101	12	CNS0021J	AL061936 Drosophil
5	119.6	4.8	1101	12	CNS00EO7	AL069440 Drosophil
6	117.4	4.7	1101	12	CNS00EO7	AL069440 Drosophil
7	116	4.7	1101	12	CNS0039G	AL063921 Drosophil
8	114.6	4.6	1190	12	CNS020N7	AL206908 Tetraodon
9	113.2	4.6	1101	12	CNS0021J	AL061936 Drosophil
10	112.8	4.6	1101	12	CNS001T2	AL078714 Drosophil
11	112.6	4.6	1169	12	CNS06KHQ	AL402900 T3 end of
12	110.8	4.5	1101	12	CNS00Z2U	AL097152 Drosophil
13	110.4	4.5	994	12	CNS04NOJ	AL298972 Tetraodon
14	110.4	4.5	1101	12	CNS003BD	AL064091 Drosophil
15	110.4	4.5	1161	12	CNS073Y8	AL428118 clone BA0
16	109.6	4.4	1101	12	CNS00BO1	AL057419 Drosophil
17	109.6	4.4	1225	12	CNS0161D	AL106171 Drosophil

18	109.4	4.4	994	12	CNS04NOJ	AL298972 Tetraodon
19	109.4	4.4	1101	12	CNS00EVL	AL071206 Drosophil
20	109.4	4.4	1101	12	CNS00KAE	AL077628 Drosophil
21	109.2	4.4	876	12	CNS009G1	AL053529 Drosophil
22	107.2	4.3	889	12	CNS006W4	AL065999 Drosophil
23	106.8	4.3	1101	12	CNS001FB	AL060732 Drosophil
24	106.4	4.3	876	12	CNS009G1	AL053529 Drosophil
25	106.4	4.3	887	10	BF274559	BF274559 GA_Eb002
26	106	4.3	1101	12	CNS00LT2	AL078714 Drosophil
27	106	4.3	1125	9	AL547503	AL547503 AL547503
28	105.4	4.3	889	12	CNS006W4	AL065999 Drosophil
29	105.4	4.3	996	12	CNS00FUH	AL071063 Drosophil
30	105.2	4.3	1161	12	CNS073Y8	AL428118 clone BA0
31	104.8	4.2	781	12	CNS009DO	AL053444 Drosophil
32	104.6	4.2	1101	12	CNS003BD	AL064091 Drosophil
33	104.2	4.2	1101	12	CNS017V2	AL108536 Drosophil
34	103.2	4.2	1125	9	AL547503	AL547503 AL547503
35	103	4.2	905	12	CNS00KHQ	AL077798 Drosophil
36	102.8	4.2	1378	12	AG031694	AG031694 Pan trogl
37	102.6	4.1	1013	12	CNS06RPQ	AL412260 T7 end of
38	102.6	4.1	1190	12	CNS020N7	AL206908 Tetraodon
39	102.2	4.1	734	12	CNS010MP	AL099163 Drosophil
40	102.2	4.1	1225	12	CNS0161D	AL106171 Drosophil
41	102	4.1	1201	12	CNS0167M	AL106396 Drosophil
42	101.8	4.1	769	12	CNS005XX	AL062647 Drosophil
43	101.6	4.1	1200	12	CNS016CO	AL106578 Drosophil
44	101	4.1	1001	12	CNS0155H	AL105023 Drosophil
45	101	4.1	1143	9	AL565457	AL565457 AL565457

ALIGNMENTS

RESULT 1

CNS00EVL

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999  
Drosophila melanogaster genome survey sequence T7 end of BAC:  
BAC29B23 of RPCI-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
AL069706  
GSS.  
AL069706.1 GI:4949849  
fruit fly.  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)  
Genoscope.  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
Aaron Mammoser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCI-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
p1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
Location/Qualifiers  
1. .1101  
/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="RPCI-98"

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/clone="BACR29B23"
/notes="end : T7"
BASE COUNT 419 a 91 c 60 g 299 t 232 others
ORIGIN

Query Match 5.3%; Score 132; DB 12; Length 1101;
Best Local Similarity 36.5%; Pred. No. 6e-07;
Matches 226; Conservative 129; Mismatches 261; Indels 4; Gaps 1;

QY 1131 ccactgacgcgactcaacaactcgaattgaattgaagcattgtagtataaggag 1190
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 439 CSCCMWMMHMAATYCTCAHTTMMWMMWMAATTTWMAAANAATTTATWATWAAA 498

QY 1191 tctagaataattctctaaattattagaggaaactatttttaaaaaattacaagaaagt 1250
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 499 AAWAWMMWATTTTMMWMTWATTTTMMWMTWATTAATAAAAAAANAATTTAAAW 558

QY 1251 ttgatcataactcttttaaaactttaattataacttaacaactttcttgactcacattgt 1310
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 559 AATAWATTAAWAATTTAAWAMMTATATTAATWTTATAAATWMTATATAAAAAATAT 618

QY 1311 gtgtaggggatttctgcaaaatatctgtctattttatactactagtagtattgtctgcg 1370
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 619 TTTTWTAAATTTTAAATTAATTTAATTAATTAATTAATTAATTAATTAATTAAT 678

QY 1371 aattatatattgattactctgggaatgattgccttaataagttataaaaaaggagaaa 1430
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 679 AATTTWAAATTAWAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANA 738

QY 1431 atattttattcataaaa----aaatacacttaataagtagtaacataataaaaaacattat 1486
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 739 AWAANAATTAWMAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 798

QY 1487 aaagagattaagtaatttaataagtagtgaattgtagaataaatttttatttataaaattt 1546
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 799 AWAANAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 858

QY 1547 gaactaaataattcaataatattcctaagtaataataagtagatataattcattcaataac 1606
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 859 AATATWAAATTAWAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANA 918

QY 1607 gactaaattcattataatcatatattagataaataatacaaaattttgtttaaatttt 1666
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 919 AAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 978

QY 1667 acattattattactaataataattcattcttgaatactctttcatacaagtaggta 1726
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 979 AWTWTATATATATATWTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1038

QY 1727 gactagaagaattatcttat 1746
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1039 TWATAWMTATATATAWAAW 1058

RESULT 2
CNS00EVL/c 1101 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
DEFINITION BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069706
VERSION AL069706.1 GI:4949849
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Direct Submission
TITLE Genoscope.
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammosser in Piter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
    source
    1. 1101
    /organism="Drosophila melanogaster"
    /db_xref="taxon:7227"
    /clone.lib="RPCI-98"
    /clone="BACR29B23"
    /notes="end : T7"

BASE COUNT 419 a 91 c 60 g 299 t 232 others
ORIGIN

Query Match 5.3%; Score 130.6; DB 12; Length 1101;
Best Local Similarity 38.1%; Pred. No. 8.8e-07;
Matches 242; Conservative 122; Mismatches 266; Indels 5; Gaps 2;

QY 1145 tacacaatctcaactgtaataatgaagcattgtagtataaggagctagaataaaattt 1204
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1100 TWWATWTTTWTWTWTWTATWTTAWATATATAAATTAATTTWTTATATATWTAWWTAT 1041

QY 1205 cttaaatattagaggaaactatttttaaaaaattacaagaaagtttgactataaact 1264
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1040 WATATATATWTTTWTAAATATATWTTTAAATAAATATATWTTAAWATATATATAWATA 981

QY 1265 cttaacaatttaattctcaacaattttcttgcacacattgctgtagaggggat 1324
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 980 WTATAWMTWMAATWAAATWATAWATAWTTTAAATAAATAATWAWMTWTTATTTT 921

QY 1325 ttgtcaaaaataatgtctattttatactactgattgtctgcgaattatacatagta 1384
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 920 TTTTWTWTATWTTTATATATWTTWMAAANAANAANAANAANAANAANAANAANAANA 861

QY 1385 ttaacttgaggaaatgattgcctaaatagttataaaaaaggagaaaaattattcata- 1443
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 860 TTAWATTTTWTWTTWTTATATWTTATWTTATWTTWTTWTTWTTATWTTATWTTWTT 801

QY 1444 aaaaaatacacttaataagtaacaataataaaaaacattataagagagattaaagtaa 1503
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 800 WTTWATTTATWTTATWMAWMTWMAWMTWMAWMTWMAWMTWMAWMTWMAWMTWTTT 741

QY 1504 tttaataagtagtaagtagtaaaattttttattataaaatttgaaactcaaaattccaaa 1563
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 740 WTTTATTTTWTWTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 681

QY 1564 taacttcaaaagtaaaataagatataattcatcattcaa----tagagagaaatcattc 1619
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 680 TTATTTAATTAWMAWMTWMAWMTTATTTAATAAATTAATTAATTAATTAATTAATTA 621

QY 1620 tattataatcatatagataaataacaaattttgttaaaattttcacattatattatt 1679
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 620 AAATATTTTWTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 561

QY 1680 actaaatataatattcttcttgaattcttttatacaagtagtagtagtagaagaatt 1739
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 560 TTTWTTTAAATTAATTTTWTWTTTAAWMTWMAWMTWMAWMTWMAWMTWMAWMTW 501

QY 1740 atcttctctccgcatattgttagatgttaaatgt 1774

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Db 500 TTTTWTATTAATAATTTTWTWAAATTTWKKK 466

RESULT 3  
 BG309087/c  
 LOCUS  
 DEFINITION  
 HVSMEC0002A15f Hordeum vulgare seedling shoot EST library  
 HVCNDA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone  
 HVSMEC0002A15f, mRNA sequence.

ACCESSION  
 BG309087  
 VERSION  
 EST  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Hordeum vulgare  
 barley.

REFERENCE  
 AUTHORS  
 Wing, R., Close, T.J., Kleinohs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.  
 Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library Unpublished (2001)  
 On Feb 22, 2001 this sequence version replaced gi:13109934.

JOURNAL  
 COMMENT  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total hg bases = 119  
 Seq primer: AATTAACTCTCACTAAAGGG  
 High quality sequence start: 13  
 High quality sequence stop: 1088.  
 Location/Qualifiers  
 1..1152  
 /organism="Hordeum vulgare"  
 /cultivar="Morex"  
 /db\_xref="taxon:4513"  
 /clone="HVSMEC0002A15f"  
 /clone\_lib="Hordeum vulgare seedling shoot EST library  
 HVCNDA0003 (Etiolated and unstressed)"  
 /tissue\_type="Seedling shoot"  
 /lab\_host="TJCL21"  
 /note="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI;  
 Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinohs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)

542 a 31 c 101 q 438 t 40 others

BASE COUNT

**BASE COUNT**



Db 1049 MMCMCCMHWTTTTTTTTTMMAWAYACAMMAYTWTTTTTAAATTTTTTTTTTMAATA 990

QY 1336 atatgtctatttatactagtagtgatttctgcgaattatatactagtagtatttaacttggag 1395

Db 989 TYCATATTTTMAATAACAWATTTTWTATACATAAATTTTWTATATACATAAATTTTAA 930

QY 1396 aaatgatgcctaagaattataaaagagagaaattatttattcattcaaaaaataacac 1455

Db 929 AATAAANAATACWAAATTTTAAWAWCATTTTWTAAWWTAAATTTTAAWWTAAATTTTAAWWTAA 870

QY 1456 ttaataaagtaacataataaaacattatataagagagatttaagataatttaataagtagt 1515

Db 869 WTAAAAAATTTTAAATAAANAARWATTAWAATTTTAYATWATATTAATTAATTAATTA 810

QY 1516 tgaatgtagaataatttttatttataaatttgaactaaataattcaaaataattcaag 1575

Db 809 ATTATTTMMWAAATTTTATATANNATTTTWTATAAATTTTAAWWTAAATTTTAAWWTAA 750

QY 1576 taaataagataataattcattcatcaacagtagtaattcaactcatttataatcatatat 1635

Db 749 TAAATAAAAAATTTTATTTTATTTTATTTTAAWWTAAATTTTAAWWTAAATTTTAAAT 690

QY 1636 tagataaataacaaatatttcttaaaattttacattattattactaaataatattataa 1695

Db 689 AATTAATAATTTTAAAWAAATTAATTTAAATAATTTTAAATTTTAAATTTTAAATTTTAA 630

QY 1696 ttcttctgaatactcttttatacaagtagtagactagaagaattatcttctatccogtat 1755

Db 629 MADWTATATANNATTTTMMWCWTWAAATATATAAATAAATAAATAAATAAATAAATAA 570

QY 1756 attttagatgtaaatg-----taacggccttagactgattttttagtattatt 1807

Db 569 WAAATAAANAATTTTATTTTATTAANWAAATTTTAAWWTAAATTTTAAWWTAAATTTTAA 510

QY 1808 atttataacatcattagagatttaagtagtaattgctctctcttcttatttaacattggtctaa 1867

Db 509 TTTTAAATTTTAT 450

QY 1868 aaatt 1872

Db 449 WTATT 445

RESULT 6

LOCUS CNS00E07

DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL069440.1 GI:4949583

VERSION AL069440

KEYWORDS GSS.

SOURCE fruit fly.

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)

AUTHORS Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the

1101 bp DNA linear GSS 04-JUN-1999

Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL069440.1 GI:4949583

GSS.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

source

1..1101

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/clone\_lib="RPCI-98"

/clone="BACR29P01"

/note="end : TET3"

BASE COUNT 366 a 66 c 104 g 351 t 214 others

ORIGIN

Query Match 4.7%; Score 117.4; DB 12; Length 1101;  
 Best Local Similarity 40.3%; Pred No. 3 le-05;  
 Matches 255; Conservative 93; Mismatches 277; Indels 7; Gaps 2;

QY 1189 agctagaataaattctttaaataattagaggaaacactatttttaaaaaattacaagaaa 1248

Db 410 AGAGDAAAAAACAATKAAWAAARRGGGKAAATATWTTKGAAGAATATAAAAAA 469

QY 1249 gtttgatctataccctcttaaaccttaaaccttaacattatctcaacaatttcttgactcacatt 1308

Db 470 RATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 529

QY 1309 gtttgataggggtgatttctcaaaatatatgctatttatacttagtagtattgtctg 1368

Db 530 WTTAAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 599

QY 1369 cgaattatatacttagtatttaacattggagaatgattgccttaaatagttata---aaaaag 1425

Db 590 TTTAAATTTATATATTAAAGWAAATAAATTAATTAATTAATTAATTAATTAATTT 649

QY 1426 agaaaattatttattcataaaaaaatacacattaaataagtaacaataataaaaaacatta 1485

Db 650 TAAATAAATTTATTTAAATTAATTTAAATTAATTTAAATTAATTTAAATTTAAATTA 709

QY 1486 tataagagattagaataatttaagtagtattgaatagaataatttttatttataaatt 1545

Db 710 AAATTTTAAATTAATAAATAAATAAATAAATTTTTTAAATTAATAAATTAATAATTAAT 769

QY 1546 tgaactaaataattcaataattcattcaagtaataataatagataataatcatcattcaata 1605

Db 770 AAATTTTAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 829

QY 1606 cgaatt---aattcaactcattataatcattatagataataataataataattttttaa 1661

Db 830 TAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 889

QY 1662 atttcatattattattactaaataattataatttcttcttgaatacttcttatacaagt 1721

Db 890 WTTAAATAAATAATGTTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT 949

QY 1722 aggtgactagaagaattattcttctcctgatatattttagatgtagttaaagttaacggc 1781

Db 950 WATTATGATATAAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 1009

QY 1782 tttagactgattttttagtattattattattattattattattattattattattattatt 1813

Db 1010 AAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 1041

## RESULT 7

CNS0039G/c

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC #

BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION

AL063921

VERSION

AL063921.1 GI:4941778

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999

Drosophila melanogaster genome survey sequence TET3 end of BAC #

BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

ACCESSION

AL063921

VERSION

AL063921.1 GI:4941778







COMMENT	Determination of this BAC-end sequence was carried out as part of a







[illegible]

JOURNAL yeast species for molecular evolution studies  
MEDLINE FEBS Lett. 487 (!), 3-12 (2000)  
REFERENCE 20584711

AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,  
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :  
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen  
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces  
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,  
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces  
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia  
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,  
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to  
5 kb were prepared and both extremities were sequenced. See  
keywords for description of this sequence and for the sequence of  
the other extremity of this insert.

FEATURES Location/Qualifiers  
source . ll161  
    /organism="Kluyveromyces lactis"  
    /strain="CLIB 210"  
    /variety="lactis"  
    /db\_xref="taxon:28985"  
    /cclone="BAOAB02G11"  
    /clone\_lib="BAOAB"

BASE COUNT         379 a                  32 c         81 g         508 t         161 others

ORIGIN

Query Match                 4.5%; Score 110.4; DB 12; Length 1161;  
Best Local Similarity      40.9%; Pred. No. 0.0002;  
Matches 407; Conservative 88; Mismatches 474; Indels 27; Gaps 5;

QY 991 agactcattggagatcttagtggtccataaaattttagaaggcgtaagttaaagtttat 1050  
| | | | | : | : | : |||| | | | | | | | | | | : | | | | |  
Db 139 AAWATAATARADADDTTTATTATTATTAAAGTAGTAATAAAXAVACATGTAAAA 198  
| | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 1051 gaasaagattggtgcattccaattaattagtttgtgaattgatgcacaatttcattcatgag 1110  
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Db 199 TTTTTTAATAATTANTATAAKATAKVGGSGGGGATATATATATATTATSSGGSSSA 258  
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QY 1171 aagcattgtagtaagaggagctagataaaattctctaattattag-aggaanaactattt 1229  
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Db 486 AAAAATATNTTATNTTNWANAAAAAWAAAAAAGGGGGGGGRARKAAANNTTTTR 545  
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QY 1410 taagtataaaaaagagaaataattattctataaaaaaaaaatacaccttaataaagtaaca 1469  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 01:59:05 ; Search time 96.17 Seconds  
(without alignments)  
6318.990 Million cell updates/sec

Title: US-09-763-957-3  
Perfect score: 2474  
Sequence: 1 ttacagatcacagaatcag.....taaccatcacaccatg 2474

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgn2.6/ptodata/2/ina/5B\_COMB.seq.\*  
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5: /cgn2.6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2.6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91.4	3.7	1511	1	US-07-991-867B-8
2	91.4	3.7	1511	1	US-08-107-755A-8
3	91.4	3.7	1511	2	US-08-544-332-8
C 4	88.6	3.6	636	4	US-08-998-416-1137
C 5	88.2	3.6	837	4	US-08-998-416-288
C 6	88.2	3.6	19124	2	US-08-487-826B-13
C 7	87.6	3.5	8920	2	US-08-446-855A-1
C 8	87.6	3.5	8920	4	US-09-150-741-1
C 9	84.2	3.4	19124	2	US-08-487-826B-13
C 10	83.4	3.4	615	4	US-08-998-416-186
C 11	81.6	3.3	636	4	US-08-998-416-1137
C 12	80	3.2	615	4	US-08-998-416-186
C 13	79.8	3.2	837	4	US-08-998-416-288
C 14	79.2	3.2	51952	3	US-08-947-823-1
C 15	78.8	3.2	665	2	US-08-883-795A-36
C 16	78.6	3.2	6243	2	US-09-056-075-1
C 17	77.4	3.1	665	2	US-08-883-795A-36
C 18	74.4	3.0	6124	4	US-08-213-419B-3
C 19	74	3.0	658	4	US-08-998-416-595
C 20	73.4	3.0	1431	4	US-09-316-083-2
C 21	73	3.0	3701	4	US-08-845-258-10
C 22	73	3.0	3701	4	US-08-990-571-10
C 23	73	3.0	3701	4	US-08-723-142A-10
C 24	72.8	2.9	6152	4	US-08-973-462-1
C 25	72.6	2.9	1431	4	US-09-316-083-2
C 26	72.6	2.9	7218	1	US-08-232-463-14
C 27	72.4	2.9	660	1	US-07-991-867B-32

28	72.4	2.9	660	1	US-08-107-755A-32	Sequence 32, Appl
29	72.4	2.9	660	2	US-08-544-332-32	Sequence 32, Appl
30	72.4	2.9	4810	3	US-08-852-629-11	Sequence 11, Appl
31	72.4	2.9	4838	3	US-08-852-629-15	Sequence 15, Appl
C 32	71.6	2.9	6124	4	US-08-213-419B-3	Sequence 3, Appl1
C 33	71.4	2.9	834	4	US-08-998-416-305	Sequence 305, App
C 34	70.4	2.8	658	4	US-08-998-416-595	Sequence 595, App
C 35	70	2.8	828	4	US-08-998-416-538	Sequence 538, App
C 36	70	2.8	6243	2	US-09-056-075-1	Sequence 1, Appl1
C 37	69.8	2.8	854	4	US-08-998-416-534	Sequence 534, App
C 38	69.2	2.8	5852	1	US-07-867-106-2	Sequence 2, Appl1
C 39	68.8	2.8	2430	4	US-08-845-258-3	Sequence 3, Appl1
C 40	68.8	2.8	2430	4	US-08-845-258-40	Sequence 40, Appl
C 41	68.8	2.8	2430	4	US-08-990-571-3	Sequence 3, Appl1
C 42	68.8	2.8	2430	4	US-08-990-571-40	Sequence 40, Appl
C 43	68.8	2.8	2430	4	US-08-723-142A-3	Sequence 3, Appl1
C 44	68.8	2.8	2430	4	US-08-723-142A-40	Sequence 40, Appl
C 45	68.6	2.8	834	4	US-08-998-416-305	Sequence 305, App

ALIGNMENTS

RESULT 1  
US-07-991-867B-8  
; Sequence 8, Application US/07991867B  
; Patent No. 5476781  
; GENERAL INFORMATION:  
; APPLICANT: Moyer, Richard W.  
; APPLICANT: Hall, Richard L.  
; APPLICANT: Gruidl, Michael E.  
; TITLE OF INVENTION: No. 5476781e1 Entomopoxvirus Expression System  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/991,867B  
; FILING DATE: 12-DEC-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO 92/14818  
; FILING DATE: 12-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/827,685  
; FILING DATE: 30-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/657,584  
; FILING DATE: 19-FEB-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UF114.C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1511 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:



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; NAME/KEY: CDS
; LOCATION: complement (234..782)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 852..1511
US-08-107-755A-8

Query Match      3.7%; Score 91.4; DB 1; Length 1511;
Best Local Similarity 44.8%; Pred. No. 9e-09;
Matches 501; Conservative 0; Mismatches 596; Indels 22; Gaps 3;

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QY 785 gaaataaacttaactactactattagtgaaattcattatgatacattcaattccaatg 844
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QY 845 tgaattcaattttccccaagattgaaagttggttgcactctgtaactaaagttgta 904
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QY 905 ttataaggtgacacatttaa-----cctaaactattttgaattgaagggtt 953
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QY 1134 cctgacgcgactacaacaatctcaatgttaattaatgagcattgtatgataaaggagct 1193
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QY 1194 agaataaattcttaaatattaggggaaaaacatcttttataaaaaattacaagaaagttg 1253
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QY 1254 atctataacctcttaaacctttaattctcaacaatttcttatgactcacattgtgtt 1313
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QY 1494 ataaagataatttaagtaagttgaataatttttatttataaaatttgaactaa 1553
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QY 1554 aattattcaataatttcaaaagtaataatagatataaattcatctattcaatcacagtaat 1613
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Query Match 3.5%; Score 87.6; DB 4; Length 8920;  
Best Local Similarity 44.7%; Pred. No. 5.5e-08;  
Matches 482; Conservative 0; Mismatches 579; Indels 17; Gaps 3;  
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Db 978 GTTGTCATAATGTAACACATTAATAATATATATATATATATATATATATATAT 1037  
QY 1340 gtctattttactagtagattgtctcggaattatataatagatttaacttggagaat 1399  
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Db 1518 AACCACTAGATAAATAGAGAGAAACGT 1546

RESULT 10  
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; Sequence 186, Application US/08998416  
; Patent No. 6239264  
; GENERAL INFORMATION:  
; APPLICANT: Philippsen, Peter  
; APPLICANT: Pohlmann, Rainer  
; APPLICANT: Steiner, Sabine  
; APPLICANT: Mohr, Christine  
; APPLICANT: Wendland, Jurgen  
; APPLICANT: Knechtle, Philipp  
; APPLICANT: Reibischung, Corinne  
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII  
; NUMBER OF SEQUENCES: 1152  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: No. 6239264artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: No. 6239264th Carolina  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/998,416

; FILING DATE: 24-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CH 0016/97  
; FILING DATE: 31-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 186:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 615 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: PAG1074RP  
; US-08-998-416-186

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QY 1476 aaaaacattataaagagattaaagataaatttaataagatttgaattagataatttt 1535  
Db 523 ATATAATTTTAAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 464  
QY 1536 ttataaatttgaactaaaataattcaaaataattcaaaagtaataataagataataatca 1595  
Db 463 AATAAATTTCTTTTAAAGTTAAATAATAATAATAATAATAATAATAATAATAATA 404  
QY 1596 tcattcaatacagagtaattcaatctattataatcaatataatagataataacaaatatt 1655  
Db 403 TATTATAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 344  
QY 1656 tgttaaatattacattattataataataataataataataataataataataataata 1715  
Db 343 ATATATATTTTAAATAAACAATTAATAATAATAATAATAATAATAATAATAATA 284  
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QY 1836 aatgtctctcttggatttttaacatggttctcaaaaataggtttcaatcgcctcctcaa 1895  
Db 164 TGATGAATTAAGTAAATATATATAATAATAATAATAATAATAATAATAATAATA 105  
QY 1896 t 1896  
Db 104 T 104  
RESULT 11  
US-08-998-416-1137  
; Sequence 1137, Application US/08998416  
; Patent No. 6239264  
; GENERAL INFORMATION:  
; APPLICANT: Philippsen, Peter  
; APPLICANT: Pohlmann, Rainer  
; APPLICANT: Steiner, Sabine

```

1  APPLICANT:  Mohr, Christine
2  APPLICANT:  Wendland, Jurgen
3  APPLICANT:  Knechtle, Philipp
4  APPLICANT:  Rebeschung, Corinne
5  TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
6  TITLE OF INVENTION:  AND USES THEREOF
7  NUMBER OF SEQUENCES:  1152
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE:  No. 6239264artis Corporation
10 STREET:  3054 Cornwallis Road
11 CITY:  Research Triangle Park
12 STATE:  No. 6239264th Carolina
13 COUNTRY:  USA
14 ZIP:  27709
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE:  Floppy disk
18 COMPUTER:  IBM PC Compatible
19 OPERATING SYSTEM:  PC-DOS/MS-DOS
20 SOFTWARE:  Patentin Release #1.0, Version #1.30
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER:  US/08/998,416
24 FILING DATE:  24-DEC-1997
25 CLASSIFICATION:  435
26
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER:  CH 0016/97
29 FILING DATE:  31-DEC-1996
30 ATTORNEY/AGENT INFORMATION:
31 NAME:  Meigs, J. Timothy
32 REGISTRATION NUMBER:  38,241
33
34 REFERENCE/DOCKET NUMBER:  PF/5-30306/A/CGC1976
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE:  919-541-8587
37 TELEFAX:  919-541-8689
38
39 INFORMATION FOR SEQ ID NO:  1137:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH:  636 base pairs
42 TYPE:  nucleic acid
43 STRANDEDNESS:  single
44 TOPOLOGY:  linear
45
46 MOLECULE TYPE:  DNA (genomic)
47 ORIGINAL SOURCE:
48 ORGANISM:  PAGI692RP
49
50 US-08-998-416-1137

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Query Match	3.3%	Score	81.6;	DB 4;	Length	636;
Best Local Similarity	50.8%;	Pred. No.	5.1e-07;			
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					4;	

Qy	1410	taagttcataaaagagagaaata	ttttattcataaaaaatacacttaataagtaaca	1469	
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Qy	1470	ataataaaaaacattataaagagatt	aaagataatttaataagtcattgaatagataaa	1529	
Db	80	ACTATTATTATCATTTTAAATAA	TTA--ATTATTGATTATTAACTATTATATATA	137	
Qy	1530	tttttattcataaattgcaactaaa	aatctccaataataatccaagaataataatagetat	1589	
Db	138	TTATTATTAATTTACTTTAAATTC	ATCATTTATTAAATTTATATATAAAAAATAAT	197	
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Db	198	TTAATATG---	AATACTATTTTAGTCTATGTTCAAA	TTTAAATTAGTATTATTAATATT	253
Qy	1650	aatattgttaaattttacattatt	attattactaataataattatttaattttcttgaatc	1709	
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Qy	1710	ttttatacaagtaggtagactaga	aattattcttatctccgcataatttgtagatgta	1769	
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RESULT 12  
 US-08-998-416-186  
 : Sequence 186, Application US/08998416  
 : Patent No. 6239264  
 : GENERAL INFORMATION:  
 : APPLICANT: Philippen, Peter  
 : APPLICANT: Pohlmann, Rainer  
 : APPLICANT: Steiner, Sabine  
 : APPLICANT: Mohr, Christine  
 : APPLICANT: Wendland, Jurgen  
 : APPLICANT: Knechtle, Philipp  
 : APPLICANT: Rebeschung, Corinne  
 : TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPTII  
 : TITLE OF INVENTION: AND USES THEREOF  
 : NUMBER OF SEQUENCES: 1152  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: No. 6239264artis Corporation  
 : STREET: 3054 Cornwallis Road  
 : CITY: Research Triangle Park  
 : STATE: No. 6239264th Carolina  
 : COUNTRY: USA  
 : ZIP: 27709  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/998,416  
 : FILING DATE: 24-DEC-1997  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: CH 0016/97  
 : FILING DATE: 31-DEC-1996  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Meigs, J. Timothy  
 : REGISTRATION NUMBER: 38, 241  
 : REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 919-541-8587  
 : TELEFAX: 919-541-8689  
 : INFORMATION FOR SEQ ID NO: 186:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 615 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: DNA (genomic)  
 : ORIGINAL SOURCE:  
 : ORGANISM: PAG1074RP  
 : US-08-998-416-186

Query Match 3.2%; Score 80; DB 4; Length 615;  
Best Local Similarity 49.7%; Pred. No. 9.9e-07;  
Matches 294; Conservative 0; Mismatches 285; Indels

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Qy	1470	ataataaaaaacattataaagagattaaagataaatttaataaagtattgaatgtagaataa	1529
Db	80	ACTATTATTATCATTTATTAAATAATTA--ATTATTTGATTATTAACTATTATTATATAA	137
Qy	1530	tttttattataaaattgaaactaaaaataatccaataaataattcaaaagtaaaaaataatagatat	1589
Db	138	TTATTATTAATTTACTTAAATTCATCATTTATTAATTTATTTATATAATTTATAAAATAATAT	197
Qy	1590	aattcatcattcaatcagtgaaatccaactattataatcatatattagataaaatataca	1649
Db	198	TTAATATG---AATACTATTTAGTCTATGTTCAAATTTTAAATTAGTTATTAAAAATATT	253
Qy	1650	aatattgttaaatatttacattattatataactaaatatattcaattttotttgaatatc	1709
Db	254	ATTAGATATTATTATTTCTTTAAATAAATATTAAATAGATTATCAATAAATTAATATATT	313
Qy	1710	ttttataaagtaggtagactagagaattcttctatctccgtatatttggtagatgta	1769
Db	314	ATTATTATTTGTTTATTAATAATAAATA-----TATTTTATTTATTAAGAATTTAATT	366
Qy	1770	aatgtaacggcttgcactgatgttttggattattattattataaaatccacttagagatt	1829
Db	367	TATTTTAAATATTCGTAAATTTATTTTATTTATATAATAATCTATTTTATTAATAATATGTT	426
Qy	1830	taagttaatgtctctcttggattttaaacatggcttciaaaaattagggttttaaatcatgcgt	1889
Db	427	GATTTATATTATTAACTTTTATAGAATTTATTATTAATAATTTAAATTTTAACTTTAATTT	486
Qy	1890	ccccaatgaaccatgcatagttttaaagtttttggtttggacaagtgttttttatt	1949
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RESULT 13
US-08-998-416-288
; Sequence 288, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; AND USES THEREOF
; NUMBER OF SEQUENCES: 1152

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RESULT 14  
US-08-947-823-1





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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2002, 02:07:21 ; Search time 477.34 Seconds

(without alignments)

8898.576 Million cell updates/sec

Title: US-09-763-957-3

Perfect score: 2474

Sequence: 1 ttacagatacacagaatcag.....taaccacatacacatattgg 2474

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits.satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	2474	100.0	2474	21	AAZ94266	Mung bean ACC synt	
2	119.2	4.8	15548	24	ABL34155	Human immune syste	
3	110.4	4.5	6106	22	AA546429	Tumour suppressor	
4	110.4	4.5	6106	24	ABL33472	Human immune syste	
5	109.4	4.4	6175	24	ABL33307	Human immune syste	
c	6	108.2	4.4	8169	22	AA546287	Tumour suppressor
7	104.8	4.2	11996	24	ABL34493	Human metastasis a	
c	8	103.4	4.2	700	22	AAH93026	Human inflammatory
c	9	102.8	4.2	1864	8	AAH71405	Sequence of ANS-1

10	102.8	4.2	6092	24	AA561080	Human gene regulat	
11	102.8	4.2	10048	24	AA561252	Human gene regulat	
12	101.4	4.1	700	22	AAH93026	Human inflammatory	
13	101	4.1	12393	24	ABL33263	Human immune syste	
14	100.6	4.1	7676	24	ABL34598	Human metastasis a	
15	99.8	4.0	6123	24	ABL32821	Human immune syste	
c	16	99.2	4.0	15548	24	ABL34155	Human immune syste
17	99	4.0	5992	24	AA561208	Human gene regulat	
18	99	4.0	7461	24	ABL33784	Human immune syste	
19	98.4	4.0	19787	24	ABL33451	Human immune syste	
20	97.8	4.0	5979	22	AA545313	Chemically pretrea	
21	97.6	3.9	8305	24	ABL33569	Human immune syste	
c	22	97.6	3.9	18624	24	ABL33702	Human immune syste
23	97.4	3.9	6071	24	ABL32325	Human immune syste	
24	97.4	3.9	6071	24	AA561076	Human gene regulat	
25	97.2	3.9	8246	24	ABL32202	Human immune syste	
c	26	96.8	3.9	4590	7	AAH60472	Sequence encoding
27	96.6	3.9	17280	22	AA546771	Tumour suppressor	
28	96.6	3.9	18624	24	ABL33702	Human immune syste	
29	96.4	3.9	5413	22	AA546694	Tumour suppressor	
c	30	96.4	3.9	5641	24	ABL33397	Human immune syste
31	96.4	3.9	13584	24	ABL32615	Human immune syste	
c	32	96.2	3.9	7597	22	ABL33013	Human immune syste
33	96.2	3.9	15732	22	AA545388	Chemically pretrea	
34	95.4	3.9	61020	22	AA546788	Tumour suppressor	
c	35	95.2	3.8	14919	22	AA546506	Tumour suppressor
36	95	3.8	9810	24	ABL32427	Human immune syste	
37	94.8	3.8	5748	24	ABL33143	Human immune syste	
c	38	94.8	3.8	6106	22	AA546429	Tumour suppressor
c	39	94.8	3.8	6106	24	ABL33472	Human immune syste
40	94.8	3.8	9155	24	ABL32463	Human immune syste	
41	94.6	3.8	8310	20	AAZ29911	CDNA encoding a SC	
42	94.2	3.8	5999	24	ABL32853	Human immune syste	
c	43	93.8	3.8	18218	24	ABL33949	Human immune syste
c	44	93.6	3.8	6641	24	ABL32315	Human immune syste
45	93.4	3.8	6131	24	ABL32890	Human immune syste	

ALIGNMENTS

RESULT 1  
AAZ94266  
ID AAZ94266 standard; DNA; 2474 BP.  
XX AC AAZ94266;  
XX DT 03-JUL-2000 (first entry)  
XX DE Mung bean ACC synthase AIM-1 gene promoter pGEL-1.  
XX KW Mung bean; 1-aminocyclopropane-1-carboxylic acid synthase;  
KW ACC synthase; AIM-1; promoter; pGEL-1; transgenic plant; ds.  
XX OS Vigna radiata.  
XX PN WO200012714-A1.  
XX PD 09-MAR-2000.  
XX PF 31-AUG-1999; 99WO-AU00705.  
XX PR 31-AUG-1998; 98AU-0005572.  
XX PA (UYUQ ) UNIV QUEENSLAND.  
XX PI Botella Mesa JR, Cazzonelli CI;  
XX DR WPI; 2000-270821/23.  
XX PT Isolated nucleic acid molecule for producing transgenic plants having  
PT altered characteristics such as resistance to a plant pathogen  
PT comprises promoter, inducible in response to physical stimulation -

XX Claim 5; Fig 4i-ii; l1lpp; English.  
XX The present sequence is that of the promoter, termed pGEL-1, of the  
CC mung bean 1-aminocyclopropane-1-carboxylic acid synthase gene, AIM-1.  
CC AIM-1 was identified as a mechanical strain-induced gene, and the  
CC promoter was cloned using a long distance inversion PCR procedure.  
CC pGEL-1 is capable of induction by physical and/or environmental  
CC stimuli in cells in which it is indigenous and, in the absence of  
CC any negative regulatory mechanism, is capable of constitutive  
CC expression in cells in which it is non-indigenous. The invention  
CC relates to this promoter, and also to derivatives of the promoter  
CC including modular forms which are, for example, inducible by  
CC different physical and environmental stimuli or which are  
CC constitutively expressed. The promoter can be used to direct  
CC expression of genes conferring useful traits on plants, such as  
CC improved resistance to a plant pathogen, altered nutritional  
CC characteristics, expression of a plantabody, altered biochemical  
CC pathway, altered fertility, and/or altered flower colour.  
XX  
XX Sequence 2474 BP; 844 A; 372 C; 363 G; 895 T; 0 other;  
SQ

Query Match 100.0%; Score 2474; DB 21; Length 2474;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 gttgaaagtttcagaaatcatgatttgattttacgtttatataaaatgaaagtgaatc 180

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Qy 1141 cgactacaacaatctcaattgtttaatttaaggaattgtagtataaaggagttctagaataa 1200  
Db 1141 cgactacaacaatctcaattgtttaatttaaggaattgtagtataaaggagttctagaataa 1200  
Qy 1201 atttcttaaatatttagaggaataactatttttaaaaaataacagaagaaagtttgactata 1260  
Db 1201 atttcttaaatatttagaggaataactatttttaaaaaataacagaagaaagtttgactata 1260  
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Qy 1321 tgattttgcgaataatatactctatttttactactagtagtgattgtctgcgaattatata 1380  
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[illegible]

RESULT 3  
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ID AAS46429 standard; DNA; 6106 BP.  
XX  
XX AAS46429;  
XX  
XX AC  
XX  
XX  
DT 18-DEC-2001 (first entry)  
DE  
DE Tumour suppressor gene derived chemically modified sequence #151.

KW	Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
KW	cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW	cytosine methylation; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200168912-A2.
XX	
PD	20-SEP-2001.
XX	
PF	15-MAR-2001; 2001WO-EP02955.
XX	
PR	15-MAR-2000; 2000DE-1013847.
PR	06-APR-2000; 2000DE-1019058.
PR	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K;
PI	
DR	WPI: 2001-602752/68.
XX	
PT	Fragments of chemically modified genes associated with tumour suppressor
PT	genes and oncogenes, useful in designing primers and probes for
PT	analysing diseases associated with cytosine methylation state e.g.
PT	cancer -
XX	
PS	Claim 1; SEQ ID No 151; 27pp; English.
XX	
CC	The invention relates to a nucleic acid comprising a sequence of 18
CC	bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC	bisulphite, of genes associated with tumour suppression and
CC	oncogenes having a sequence taken from 536 (actually 533 since
CC	numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC	(SS) and sequences complementary to (SS). The nucleic acid may be a
CC	peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC	form part of a set of probes for detecting the cytosine methylation state
CC	and/or single nucleotide polymorphisms and also to be used in an
CC	array for analysing diseases associated with CpG dinucleotides e.g.
CC	cancers and tumours. The probes can also be used in a method for
CC	ascertaining genetic and/or epigenetic parameters for the diagnosis
CC	and/or therapy of existing diseases or the predisposition to specific
CC	diseases, by analysing cytosine methylations. The parameters may be
CC	compared to another set of genetic and/or epigenetic parameters, the
CC	differences serving as basis for diagnosis and/or prognosis events which
CC	are disadvantageous to patients. The present sequence is one of the
CC	533 genomic sequences derived from tumour suppressor genes and
CC	oncogenes.
CC	
CC	Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic
CC	format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 6106 BP: 1938 A; 30 C; 849 G; 3289 T; 0 other;

Query Match	4.5%	Score 110.4;	DB 22;	Length 6106;
Best Local Similarity	45.1%	Pred. No. 1.9e-07;		
Matches 579;	Conservative	0;	Mismatches 691;	
			Indels 14;	Gaps 4;

Qy	673	ttaatttattttttaatttatgcatttgatttataataaaccaattatggtatgatt	732
Db	4194	ttaaattatttttttttttttttgagatttgatttataaagtattttatttatattt	4253
Qy	733	aagtcgtatatogtgcacattgaagttttctcgaagtttgccattttatgaaataa	792
Db	4254	atttttttttaatttggttcaaaatat-tgaaaataatttttttttggaataa	4312
Qy	793	acttaactactactataggtaaattcatatgatacatcaacaattccaatggagtca	852
Db	4313	tttttttataataataattgaattcaatttgcaagataataaataatgaatttttaa	4372

Qy	1926	tgttttggacaatggtttttatt	1949
Dd	5447	tattgtacgttaagtattgtttt	5470
 RESULT 4			
ABL33472			
ID	ABL33472 standard; DNA; 6106 BP.		
XX	AC AC		
XX	ABL33472;		
XX	26-MAR-2002 (first entry)		
DF			
XX			
DE	Human immune system associated gene SEQ ID NO: 1445.		
XX			
KW	Human; Immune system disease; cytosine methylation; antiasthmatic;		
KW	antiarteriosclerotic; antianaemic; cytostatic; nootropic;		
KW	neuroprotective; anti-HIV; anticongulsant; ophthalmological;		
KW	antirheumatic; antiarthritis; antidiabetic; antipsoriatic;		
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;		
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;		
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;		
KW	gene; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200200928-A2.		
XX			
PD	03-JAN-2002.		
XX			
PF	02-JUL-2001; 2001WO-EP07537.		
XX			
PR	30-JUN-2000; 2000DE-1032529.		
PR	01-SEP-2000; 2000DE-1043826.		
XX			
PA	(EPIG-) EPIGENOMICS AG.		
XX			
PI	Olek A, Piepenbrock C, Berlin K;		
XX			
DR	WPI; 2002-130909/17.		
XX			
PT	Nucleic acid comprising fragment of chemically modified gene, useful		
PT	for diagnosis and treatment of diseases associated with abnormal		
PT	cytosine methylation		
XX			
PS	Claim 1; SEQ ID NO 1445; 32pp + Sequence Listing; German.		
XX			
CC	The present invention provides a number of human immune system associa-		
CC	genes which are modified by the methylation of cytosines. The sequence,		
CC	can be used in the diagnosis and treatment of immune system disorders,		
CC	including eye diseases such as retinopathy, neovascular glaucoma and		
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid		
CC	leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,		
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel		
CC	diseases. The present sequence is a gene of the invention.		
XX			
SQ	Sequence 6106 BP; 1938 A; 30 C; 849 G; 3289 T; 0 other;		
Query Match 4.5%; Score 110.4; DB 24; Length 6106;			
Best Local Similarity 45.1%; Pred. No. 1.9e-07;			
Matches 579; Conservative 0; Mismatches 691; Indels 14; Gaps			
Qy	673	ttaatttatttttaattgatcgaatttgatcttatataaaacaattatggtatgatt	732
Dd	4194	ttaatttatttttttttttgtagagtttagttatttcataaaggttttatttatatt	4253
Qy	733	aagtcgtatatcggtgacaattgaaqttttctctaagtttagccaatttttatgaaattaa	792
Dd	4254	attttttttaattgtgtaaaaaat-gtgaataattatatttttgggaataaa	4312
Qy	793	acttaatcacactattagtgaaatcatatcatatcataaacaaatttcaatgttgtca	852





CC 533 genomic sequences derived from tumour suppressor genes and  
CC oncogenes.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 8169 BP; 2420 A; 116 C; 1665 G; 3960 T; 8 other;

AA	
AC	ABL34493;
XX	
DT	26-MAR-2002 (first entry)

AA	Human metastasis associated gene SEQ ID NO: 46.
DE	
XX	Metastasis associated gene; cytosstatic; gene therapy; cancer;
KW	cytosine methylation; gene; ds.
KW	
XX	Homo sapiens.
OS	
XX	
FN	WO200177376-A2.
PN	
DD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-EPO3970.
XX	
PR	06-APR-2000; 2000DE-1019058.
PR	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	
DR	WPI; 2002-010922/O1.
XX	
PT	New nucleic acid derived from chemically treated metastasis genes,
PT	useful for diagnosis of cancers by analysis of cytosine methylation,
PT	also for treatment _
XX	
PS	Claim 1; SEQ ID NO 46; 23pp + Sequence Listing; English.
XX	
CC	The present invention provides a number of human metastasis associated
CC	genes which are modified by cytosine methylation. The sequences can be
CC	used in the diagnosis and treatment of cancer. The present sequence is
CC	one of the genes of the invention.
XX	
SQ	Sequence 11996 BP; 2966 A; 261 C; 3041 G; 5728 T; 0 other;
	Query Match            4.2%; Score 104.8; DB 24; Length 11996;
	Best Local Similarity   47.9%; Pred. No. 1.1e-06;
	Matches 365; Conservative   0; Mismatches 392; Indels   5; Gaps   2;
Qy	1209 aaataggaggaacactatttttaaaaaataaccagaaggttgatctatacaacctttt 1268 
Db	10570aatgagtaagattttatttcaaaaagagaaaaaaagaaagtaatttaagatta 10629 
Qy	1269 aaacttaaaattatcacaattttcttatgcacacttgtgtgatgggtgatttg 1328 
Db	10630 ttttaattaataataattatttagtcataataataataataataattatttag 10689 
Qy	1329 tcaaaatatagtctattttatactagtagtattgtctgcgaattatatagatttaa 1388 
Db	10690 tataataataattataataattatttagtataaaaaaattattattatacaattat 10749 
Qy	1389 cttggagaaaagtgcctaataagttataaaaaagggagaaaattatttattcataaaaa 1448 
Db	10750 tatagtagtgcacaaattataataagaatttatgtataataattataataataata 10809 
Qy	1449 ataacacttaataagtaacaataataaaaaacatttatataagagagatttaagataattaa 1508 

Db	588	TAAAAACCCAAAACGAACTAATACAAAACCAAAATCAATTCCTTATATTAAAC	529
Qy	1616	aatctattataatcacatattagataaaatatacaaatatttggtaaaattttcacattatta	1675
Db	528	AACAAAATTTCTTTAAAAATATATCTAAATTTTAAATAAAATTTTAAATTTTAA	469
Qy	1676	tattactaaataLatattaat-----tcttttgaatctctttatacaagtagtagac	1729
Db	468	AAATTATACATCTATTTTAAACAAATATCTTCTCCTTTAACATCTATTTAAATTTCCATAT	409
Qy	1730	tagaagaattatcttctccggtatattgttagatgtttaaagtcaacgggcttagactg	1789
Db	408	TTTAAATTTAAAAATATATATCTTCTTAATTTAAAAATAAATTTTCATTCCTTTAAAAATCAAA	349
Qy	1790	atgctttttgtattatattttataaaccattagagattttaagtttaagtctctctctttg	1849
Db	348	TTATTTTATTTTTTTTTTTTCTCAAAATCATATTTACAAAATTCATCTTTTACAAATTC	289
Qy	1850	attttaacatggtctcaaaaatttaggtttaaatcatcttgctcctcaatgaacccatgctat	1909
Db	288	TTACTATACATAAATTTTACAAATCAATATATCATTTTCTTCATTTTTTTTCTCCCTTAAAAA	229



Db	10810	atttagtataataatcattattatacaataataattattatacaattttaagaattatcagttcat	10869
Qy	1509	taegtattgaattagataaattttttattataaatttgaactaaaattccaataata	1568
Db	10870	ataataataattataat-ttaagaattataacgtataaattataataatttaataatta	10928
Qy	1569	tccaagtaanaataatagataataattcaatcattcaatcgcggaattcaatcattataat	1628
Db	10929	tataatcgtataataattataataataatgt-aaatataataattattata	10984
Qy	1629	catattagataaataatacaaaatattgttcaaattttcaattattattactacaatat	1688
Db	10985	atagtaataattattattataataataataattattataataataatacaattat	11044
Qy	1689	atattaattcttttgaatatcttttatcaagtaggtagactagaagaattattcttct	1748
Db	11045	attataataataataataaattataattataataataataattattataataataatt	11104
Qy	1749	cccgatatatttgttagatgttaaaatgtaacgggttagactgagtcttttgtattatatta	1808
Db	11105	ataatatattagtaataattttttttagacggagttttatttttatgttttaggttgag	11164
Qy	1809	ttataaatccattagagatttaagttaagtctctctcttggatttttaacatggtctaaa	1868
Db	11165	tttaatggtcgattctcgatttattgtcattttttcattttttgggttcaagtgatttttt	11224
Qy	1869	aattaggtttaaatcatgctgcctcaatgaaccatgctatatgtttttaaagtttttgt	1928
Db	11225	gttttagttttcgagtaagtgtgggattatagggtatttgatcatcgattcggttaatttt	11284
Qy	1929	tttttgacaatgtttttattttctgagattgctcttaggatt	1970
Db	11285	ttttttttttttttttttgtatttttttagtagagatagggatt	11326

## RESULT 8

AAH93026/c  
ID AAH93026 standard; DNA; 700 BP.

AC AAH93026;

DT 09-OCT-2001 (first entry)

DE Human inflammatory bowel disease related gene fragment IGR3319a.

Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.

OS Homo sapiens.

WO200142511-A2.

14-JUN-2001

XX  
PF  
11-DEC-2000. 2000WO-PGS33632

10-DEC-1988. 0000-0170357

PR 10-APR-2000; 2000US-0196046.

PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.

XX

XX

XX

PT bowel disease, using a hybridization assay -

PS Disclosure; page 384; 463pp: English.

The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a gene containing a polymorphic site described in the exemplification of the invention.

Sequence 700 BP; 370 A; 13 C; 14 G; 302 T; 1 other;  
SQ

Query Match 4.2%; Score 103.4; DB 22; Length 700;  
Best Local Similarity 50.5%; Pred. No. 2.1e-06;  
Matches 307; Conservative 0; Mismatches 292; Indels 9; Gaps 2

Qy	1273	tttaaatattactacaacaaattttcttatgactgcacattgtgtgatggggcgatttggctcaa	1332
Db	676	TTAAATATATTAAATATATATTTAAATATATATATATATATTTAAATATATATATATATAT	617
Qy	1333	aatatatgctctattttacactagtatgattgtctgcgaattcatatagattagtaacttgc	1392
Db	616	AAATATATATTATATATTTAAATATATATATATATATTTAAATATATATATATATATATAT	557
Qy	1393	gagaaatgattgcctcaataaagtcttaaaaaaggagaaaaattttattctctcaaaaaaata	1452
Db	556	TATATATATTTAAATATATATAATATATATATATTTAAACATATTTTAAATATATATTTTAAAAATA	497
Qy	1453	cacttaaaatgaagtaacaaataaaaaaacattataaagagattaaagatacaatttaataag	1512
Db	496	TAAATTTATATATTTATATAATATATATATATATATATATATATATATATATATATATAA	437
Qy	1513	tattgaatgtagaataaattttatttataaaatttgaactcaaaatattccaataattctca	1572
Db	436	TATATAATATATATATTTATATAATAATATATATATATATATATATATATATATATTTATAT	377
Qy	1573	aagtaaaataatagatatataattcoactcaatcacgagtaactcaatcctattataatcata	1632
Db	376	ATTGTATATTTATATATTTGTATATATTTATATATATATATATATATATATATATTTTATATATAT	317
Qy	1633	tattgatacaaatatcac-----aatattgttcaaaatttcacatttatattactataa	1684
Db	316	ATATATATATTTATATATATATATATATATATTTTATATATATATTTTATATATATATATAT	257
Qy	1685	atatattaactattcttgaatatcttttatacaagtagtgtagactagaaga-attatctt	1743
Db	256	ATATATTTTATATATATTTTATATATTTTATATATTTTATATATATTTTATATATATATAT	197
Qy	1744	tatctccogtatatttggtagatgtttaaagtgaacggccttagactgagtcttttggcatca	1803
Db	196	ATATTTTATATATATTTTAT	137
Qy	1804	tattatttataaaatccactagagatttaagttaaagtctctcttggatttttaacatggctt	1863
Db	136	TTTTTATATATATTTTATATATTTACATATATATATATATATATATATATATATATATATATAT	77
Qy	1864	ctaaaaat	1871
Db	76	TTATATAT	69

## RESULT 9

RESUL  
AAN71405/C

ID AAN71405 standard; DNA; 1864 BP.

AA  
AC AAN71405;XX  
XX

DT 18-APR-1991 (first entry)

Sequence of ANS-1 which increases transformation efficiency.

Enzyme: fungal expression vector: *Aspergillus* expression vector.





Db 3278 aagggtatttagttttttatttagttgtgtgttttttaatttaatttaattttatttagtaaaagatt 3337  
Qy 1976 tatgtttgatacagaacgaagtagagtagtaggtatatacagtgtaaaaaataat 2035  
Db 3338 agtgattatgttttttaagaaaaataataaattttttgttagtgatttagttatttaatt 3397  
RESULT 11  
AAS61252  
ID AAS61252 standard; DNA; 10048 BP.  
AC AAS61252;  
XX  
DT 29-JAN-2002 (first entry)  
XX  
DE Human gene regulation-associated gene oligonucleotide #207.  
XX  
KW Human; Gene regulation-associated gene; severe combined immunodeficiency;  
KW cardiac damage; inflammatory response; Haemophilia; Werner syndrome;  
KW asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome;  
KW renal disease; Preclampsia; cardiac allograft vascular disease;  
KW colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;  
KW immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;  
KW nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177375-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-EP03968.  
XX  
PR 06-APR-2000; 2000DE-1019058.  
PR 07-APR-2000; 2000DE-1019173.  
PR 30-JUN-2000; 2000DE-1032529.  
PR 01-SEP-2000; 2000DE-1043826.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPT; 2002-017470/02.  
XX  
XX  
PT New nucleic acid sequences from chemically modified genes associated  
PT with gene regulation, useful for analysing cytosine methylations for  
PT diagnosis and therapy of diseases e.g. severe combined immunodeficiency  
PT disease -  
XX  
PS Claim 1; SEQ ID No 212; 26pp; English.  
XX  
XX  
CC The invention relates to 224 nucleic acid sequences comprising at least  
CC 18 bases of a chemically pretreated gene associated with gene regulation  
CC selected from 43 known genes (or complementary sequences): The  
CC chemical pretreatment converts cytosine bases unmethylated at the  
CC 5-position to uracil or another base with hybridisation behaviour  
CC dissimilar to cytosine, to enable analysis of cytosine methylations.  
CC The DNA sequences, oligomers (or sets/arrays) and method are  
CC useful in the diagnosis of diseases (or predisposition to diseases)  
CC associated with gene regulation and in therapy of such diseases, by  
CC enabling analysis of the cytosine methylation patterns of such genes,  
CC kits are provided. They are especially useful in diagnosis  
CC and therapy of e.g. severe combined immunodeficiency disease, cardiac  
CC disorders, haemophilia, solid tumours and cancer, Werner syndrome,  
CC asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease,  
CC preclampsia, graft versus-host disease. The present sequence is a  
CC sequence included in the sequence data for this specification and is  
CC associated with the human gene regulation-associated genes.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 10048 BP; 3493 A; 57 C; 1789 G; 4704 T; 5 other;  
Query Match 4.28; Score 102.8; DB 24; Length 10048;  
Best Local Similarity 43.8%; Pred. No. 2.2e-06;  
Matches 623; Conservative 0; Mismatches 790; Indels 8; Gaps 4;  
Qy 616 gtaagtcacaacttttctactcttatttaattgagggtattttttccatacacaatta 675  
Db 6375 gtaattaggttttttagatttaataatttaattttattttattttattttataatttt 6434  
Qy 676 atttatttttttaattttgactttttgactttttatttttttttttttttttttttttt 733  
Db 6435 ttttttttttttaatttaattttgtgtgtgagtgaggtttttttttttttttttttgaga 6494  
Qy 734 agtcgtatatcgggacaaattgaattgttttctcctaagtttttaagccattttttatgaataaaa 793  
Db 6495 atgttt 6554  
Qy 794 cttaactactactattagggttaattcatcatcatcatcaataatttcaatttgagggttcaa 853  
Db 6555 gttattttatgaaggttt 6614  
Qy 854 ttttaccacaagattgaaagtgtgttgcactttctgttaacttaaaagtgtgtattataaggt 913  
Db 6615 tatatagatttagtgaaataattatgttaacgttttttttttttttttttttttttttttt 6674  
Qy 914 tgacgactttaaccttaactctattttgaattgaagggtttgacttcgacttcgacttttaaat 973  
Db 6675 atttatttagttaaagttt 6734  
Qy 974 aattcaactaaagtcttagactacattggagattttttgtgtttctataaaatttttagaaaaa 1033  
Db 6735 atatagattttgtgttaattagtttttttttttttttttttttttttttttttttttttt 6793  
Qy 1034 ggtcgtgattaaagtattgaaaaagattggtgacttattcaatttaattggtgtgaaattgat 1093  
Db 6794 ngttgtgttttattaaagattgattgttttttttttttttttttttttttttttttttttt 6853  
Qy 1094 gacaaattttcattgacataccaatacagagaataaccacctcgacgcagctacaacaat 1153  
Db 6854 tttttatagtanttattttattttattttatttttttttttttttttttttttttttttttt 6913  
Qy 1154 ctcaattgtaatttaattgaagcattgttagtataaggagcttagaataaaattttcttaaatat 1213  
Db 6914 ttgttttaattaaaaaaaatttttagtttagtaaaagtaattatttttaaaagattgtgtat 6973  
Qy 1214 tagaggaaaactatttaact 1273  
Db 6974 tataataaatttaataataataataaagtcgtgggaaagataaagattgttttttaaaag 7033  
Qy 1274 ttaatttatcacaactttttctttagctcacattgtgtgattgaggtgtgtttgttgcataa 1333  
Db 7034 ttaaaaaaaagttttaagtttttagtaaaaaagtaaaattattaaaaagattttgtgtgataa 7093  
Qy 1334 atatatgtctattttatactagtattgtttgtcgcgaattatataatagttatttaacttgg 1393  
Db 7094 attaggtaaggttggtgaaagagaaaaattattgaagtttagaaggtgtttattattta 7153  
Qy 1394 agaaatgattgccttaataagttataaaaaagagaaaaatttttttttttttttttttttttt 1453  
Db 7154 aattgtttattattattgttt 7213  
Qy 1454 acttaataaagtaacaataat--aaaaaacattataaagagataagataataataataa 1511  
Db 7214 tttattatgagtggtgattttatttaagaagaataattgttagaatttttaaatatgtatgagat 7273  
Qy 1512 gtattgaatgtagaataatt 1571  
Db 7274 ttttttttagaaaaaggtttttgttttttttttttttttttttttttttttttttttttttt 7333  
Qy 1572 aaagttaataatagatatataatttcattcattcaacgaggttaattccaatttatataaat 1631

Db 7334 gagttaaagtgtttatagatatattttatagttatataatatatatattatagttttatgatttttta 7393  
 Qy 1632 atattgagataaaatatacacaatatttggtaaattttacattttatattattataataataata 1691  
 Db 7394 ttattaaatttaattatgttttaggttaaagggtttttttattgttaattttttgttaattgat 7453  
 Qy 1692 ttaattcttctgaatattctttttacaaagttagtagactagaagaattattcttctatccc 1751  
 Db 7454 tattatttttttagtagtggttttaaatttttgaggataagagtttagatttttaattttatag 7513  
 Qy 1752 gtatttttttagtagtggttttaaagttaacgggcttagactgagttttttttgtattattattt 1811  
 Db 7514 ttatttaattattataataattttttatataataattattattattattattattttttgtt 7573  
 Qy 1812 ataaatccattagagatttaagttaagtctctctctttttgatttttaacatggttctcaaaaat 1871  
 Db 7574 tgaatgaagtttagagagatgataaagatgggttttttttttttttttttttttttttttagt 7633  
 Qy 1872 taggtttaatcattggctctcaatgaacccatgctatgttttttaaaagtttttttttttttt 1931  
 Db 7634 aatgttgggttgaggtaaaggataaagaaatattttttattttatttta---ttttttataaa 7690  
 Qy 1932 ttgacaatgttt 1991  
 Db 7691 ttgtttaagtttcaaaagtttagaattgggttaaaggtttttttttttttttttttttttttt 7750  
 Qy 1992 aaacgagaagtagagagtagttatcacacgtgtataaaaaat 2032  
 Db 7751 gtaagaaaatt 7791

RESULT 12  
 AAH93026  
 ID AAH93026 standard; DNA; 700 BP.  
 XX  
 AC AAH93026;  
 DX  
 DT 09-OCT-2001 (first entry)  
 XX  
 DE Human inflammatory bowel disease related gene fragment IGR3319a.  
 XX  
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;  
 KW chromosome 5q31-33; forensic test; gene therapy; ds.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200142511-A2.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000WO-US33632.  
 XX  
 PR 10-DEC-1999; 99US-0170257.  
 PR 10-APR-2000; 2000US-0196046.  
 XX  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 PA (ELLIP-) ELLIPSIS BIOTHERAPEUTICS CORP.  
 XX  
 PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;  
 XX  
 DR WPI; 2001-367874/38.  
 XX  
 PT Testing for the presence of polymorphisms associated with inflammatory  
 PT bowel disease, using a hybridization assay -  
 XX  
 PS Disclosure; Page 384; 463pp; English.  
 XX  
 CC The present invention describes a method for detecting the presence of  
 CC polymorphisms associated with inflammatory bowel diseases such as  
 CC ulcerative colitis and Crohn's disease. The methods can be used to detect  
 CC the presence of genetic polymorphisms associated with inflammatory bowel  
 CC disease and correlating their occurrence with disease states. They may be

CC used in this way for phenotypic correlations, forensics, paternity  
 CC testing, medicine and genetic analysis. The present sequence is a gene  
 CC containing a polymorphic site described in the exemplification of the  
 CC invention.  
 XX  
 SQ Sequence 700 BP; 370 A; 13 C; 14 G; 302 T; 1 other;  
 Query Match 4.1%; Score 101.4; DB 22; Length 700;  
 Best Local Similarity 52.1%; Pred. No. 4.1e-06;  
 Matches 323; Conservative 0; Mismatches 287; Indels 10; Gaps 4;  
 Qy 1197 ataaattcttcaataatttagaggaactatttttaaaaaattacaagaagaattgttc 1256  
 Db 73 ataaatatataataataataataataataataataataataataataataataataata 132  
 Qy 1257 taaacaccttttaaaacttttaaaattatctaaacaattttcttactgactcacattgtgttgat 1316  
 Db 133 aaaaatatataataataataataataataataataataataataataataataataata 192  
 Qy 1317 aggggtgattttgtcaaaaatatatgtctattttttactagtagtattgtctgcgaattat 1376  
 Db 193 atataataataataaaaatatataataataataataataataataataataataata 252  
 Qy 1377 atatagatttaacctggagaaatgattgcctaataagttataaaaaaggagaaaatttt 1436  
 Db 253 atataaaaatatataataaaaatatataaaaatatataataataataataataataata 312  
 Qy 1437 attcaaaaaaaatacacacttaataagtaaca-ataataaaaaaacattataaagsgat 1495  
 Db 313 atataataataaaaatatataaaaatatataataataataataataataataataataata 372  
 Qy 1496 ta--agataatttaagaattgaaatgtagaataattttttattataaaatttgaactaa 1553  
 Db 373 caataataaataataaaaatatataataataataataataataataataataataata 432  
 Qy 1554 aatatt-caaataattcaaaagtaaatagataataatcattcattcaatacgaagtaa 1612  
 Db 433 taccattatattatattatattataataataataataataataataataataataata 492  
 Qy 1613 ttcaattattataatacatatttagataaaatacaaa-----ataattgttaaaatttt 1666  
 Db 493 ttatatttttaataataatttttaaaatgttttaataataataataataataataataata 552  
 Qy 1667 acattattattactaaataataataatttttttttttttttttttttttttttttttttt 1726  
 Db 553 tataataataataataataatttttaaaatatataataataataataataataataata 612  
 Qy 1727 gactagaagaattattctctccgtattattgttagattgttaaatgttaacgggcttaga 1786  
 Db 613 tattattattatanattataataataataataataataataataataataataataata 672  
 Qy 1787 ctgattgtttttgtattatat 1806  
 Db 673 ttaataataatttaataatat 692

RESULT 13  
 ABL33263  
 ID ABL33263 standard; DNA; 12393 BP.  
 XX  
 AC ABL33263;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human immune system associated gene SEQ ID NO: 1236.  
 XX  
 KW Human; immune system disease; cytosine methylation; antiasthmatic;  
 KW antiarteriosclerotic; anti-naemic; cytosine; cytosine; cytosine;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;











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